

STIC-Biotech/ChemLib

84063

From: Chan, Christina  
Sent: Monday, January 13, 2003 7:59 AM  
To: Minnifield, Nita; STIC-Biotech/ChemLib  
Subject: RE:

RECEIVED

JAN 13 2003

STIC-BIOTECH/CHEM LIB  
(STIC)

Please rush. Thanks Chris

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
308-3973  
CM-1, 9B19

-----Original Message-----

From: Minnifield, Nita  
Sent: Sunday, January 12, 2003 1:12 PM  
To: Chan, Christina  
Subject:

Christina,  
Please approve, 2 month amdt.

STIC

09/144886

PALM indicates "NO BIOTECH DATA"; however application file has a RSL copy with "ENTERED" stamped on it. Date on RSL is 9/1/99

Please do a commercial sequence search on SEQ ID NO:63 and 87 of the above application. Please provide a paper copy of the results.

Thanks,

Nita M. Minnifield

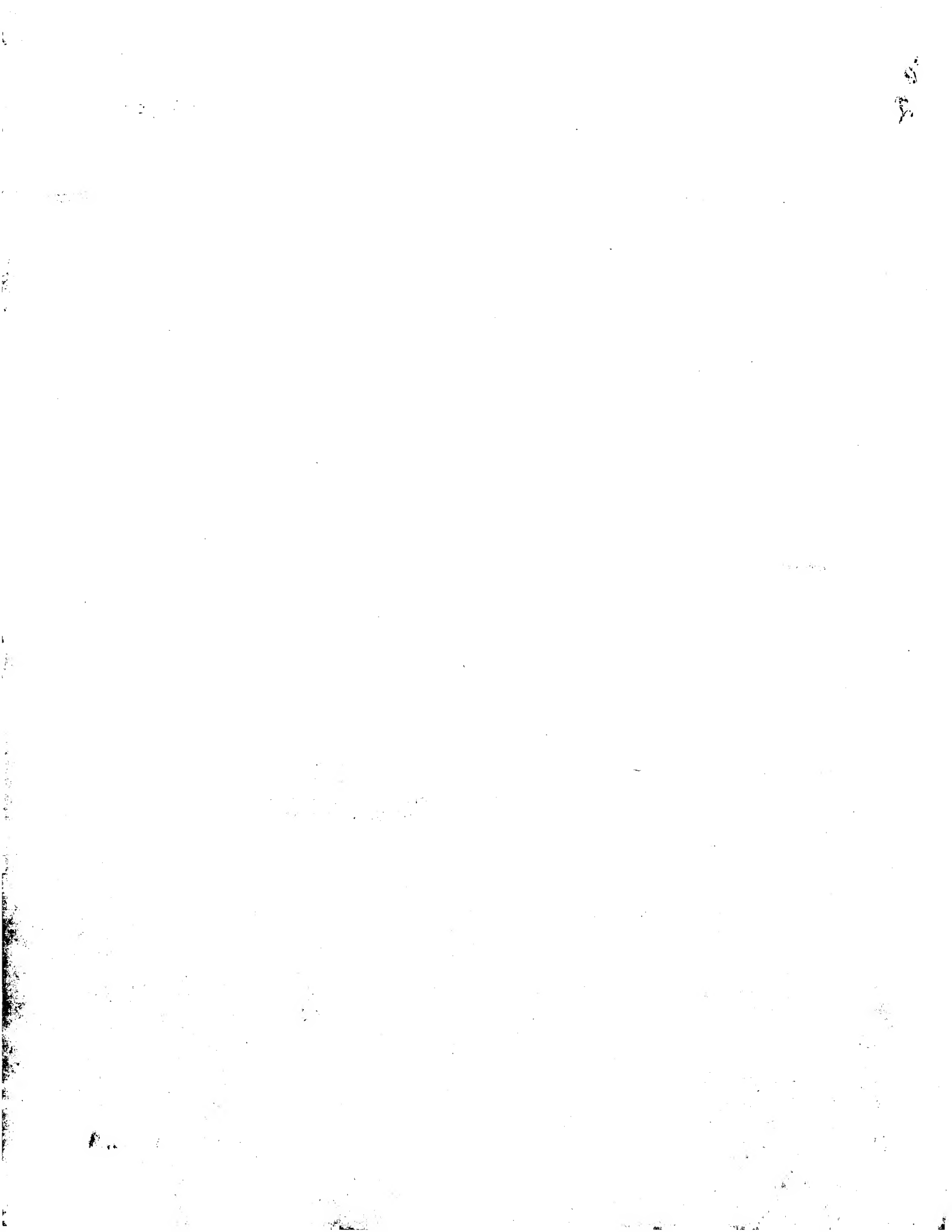
Art Unit 1645  
Office CM1-8A07  
Mailbox CM1-8E12  
703-305-3394

Point of Contact:  
Barb O'Bryen  
Technical Information Specialist  
STIC CM1 6A05 308-4291

Searcher: Bob  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 1-13-03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:10:24 : Search time 14.3652 Seconds  
(without alignments)  
789.676 Million cell updates/sec

Title: US-09-144-886-63

Perfect score: 633

Sequence: 1 QVQLQESGGGLVPRGSGSLK.....YRVDAMDYWGQGTITVYSS 118

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575.5	90.9	152	B26471	Ig heavy chain pre
2	547.5	86.5	122	E27888	Ig heavy chain v r
3	545.5	86.2	120	S55536	Ig heavy chain v r
4	544	85.9	119	D27889	Ig heavy chain v r
5	538.5	85.1	120	S55537	Ig heavy chain v r
6	538	85.0	119	B27889	Ig heavy chain v r
7	534.5	84.4	120	S55539	Ig heavy chain v r
8	533	84.2	119	E27888	Ig heavy chain v r
9	523.5	82.7	120	S55538	Ig heavy chain v r
10	517.5	81.8	118	E27889	Ig heavy chain v r
11	515	81.4	121	I27887	Ig heavy chain v r
12	510	80.6	121	S55540	Ig heavy chain v r
13	508	80.3	98	HYMS95	Ig heavy chain v r
14	506.5	80.0	119	A43413	Ig heavy chain v r
15	506	79.9	121	H27888	Ig heavy chain v r
16	502.5	79.4	138	S09258	Ig heavy chain v r
17	502	79.3	118	PH0096	Ig heavy chain v r
18	502	79.3	254	B31790	Ig heavy chain v r
19	497	78.5	118	PH0097	Ig heavy chain v r
20	495.5	78.3	118	S20641	Ig heavy chain v r
21	491	77.6	121	A27888	Ig heavy chain v r
22	491	77.6	139	S38808	Ig heavy chain v r
23	490	77.4	121	B27888	Ig heavy chain v r
24	490	77.4	121	B27887	Ig heavy chain v r
25	489	77.3	123	C27888	Ig heavy chain v r
26	487.5	77.0	124	C27888	Ig heavy chain v r
27	487	76.9	101	C27889	Ig heavy chain v r
28	484	76.5	548	S38864	Ig epsilon chain C
29	483.5	76.4	124	I27888	Ig heavy chain v r

30	483	76.3	121	2	D27888	Ig heavy chain v r
31	480.5	75.9	119	2	B34353	anti-peptide Fab'
32	477	75.4	108	2	PI0248	Ig heavy chain v r
33	477	75.4	112	2	A27889	Ig heavy chain v r
34	477	75.4	118	2	S31105	Ig heavy chain (su
35	476	75.2	123	2	S63597	Ig heavy chain v r
36	475.5	75.1	119	2	PH0098	Ig heavy chain v r
37	472	74.6	113	2	S02717	Ig heavy chain v r
38	470	74.2	113	2	S26468	Ig heavy chain v r
39	469	74.1	112	2	S26327	Ig heavy chain v r
40	467	73.8	128	2	PH0095	Ig kappa chain v r
41	465	73.5	108	2	PH1011	Ig heavy chain v r
42	464	73.3	114	2	S31120	Ig heavy chain - h
43	464	73.3	120	2	S12953	Ig heavy chain v r
44	463.5	73.2	117	2	PI0249	Ig heavy chain v r
45	463	73.1	128	2	PH0094	Ig heavy chain v r

## ALIGNMENTS

```

RESULT 1
B26471
Ig heavy chain precursor V region (MAK33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C:Accession: B26471; S70410
R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
A:Reference number: A91572; MUID:87248058; PMID:3110009
A:Accession: B26471
A:Molecule type: mRNA
A:Residues: 1-152 <BUC>
A:Cross-references: GB:M16163; NID:9195405; PIDN:AAA38292.1; PID:9195406
R:Lepecque, S.G.; Gearhart, P.J.
J. Exp. Med. 172, 1717-1727, 1990
A:Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' bound
A:Reference number: S70410; MUID:91079775; PMID:2258702
A:Accession: S70410
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-19 <LEB>
A:Cross-references: EMBL:X53776; NID:952475; PIDN:CAA37792.1; PID:952476
C:Genetics:
A:Introns: 16/1
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-152/Product: Ig heavy chain V region MAK33 #status predicted <MAT>
F:34-117/Domain: Immunoglobulin homology <IMB>

Query Match          90.9%; Score 575.5; DB 2; Length 152;
Best Local Similarity 89.4%; Pred. No. 4.3e-44;
Matches 110; Conservative 4; Mismatches 4; Indels 5; Gaps 1;

QY 1 QVQLQESGGGLVPRGSGSLSCAASGFTSDYIMRWVROTPKRLKLVATISDGSGYTY 60
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 20 EVQVGGESGGGLVPRGSLKSLSCAASGFTSDYIMRWVROTPKRLKLVATISDGSGYTY 79

QY 61 PSVKGKFTISRDNAKNNLYLQMSSILKSEDTAMVYCSR-----YDDAMDYWGQGTITV 115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80 PSVKGKFTISRDNAKNNLYLQMSSILKSEDTAMVYCARKAYGNGDAMDYWGQGTITV 139
      ||| |||

QY 116 VSS 118
      |||
DB 140 VSS 142

RESULT 2
E27888
Ig heavy chain V region (H35-C6) - mouse
C:Species: Mus musculus (house mouse)

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C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C:Accession: E27889  
R:Catlon, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A>Title: Structural and functional implications of a restricted antibody response to a  
A:Reference number: A91043; MUID:86300658; PMID:2427335  
A:Molecule type: DNA  
A:Residues: 1-122 <CAT>  
A:Experimental source: strain Balb/c  
A>Note: this sequence was determined from the germine gene  
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 547.5; DB 2; Length 122;  
Best Local Similarity 88.4%; Pred. No. 1e-41;  
Matches 107; Conservative 3; Mismatches 6; Indels 5; Gaps 2;

QY 2 VOLOESGGGLVPRGSLKLSCAASGFTFSDYYWVWVROTPERKLEWVATISDGSSTYYP 61  
|:|||||  
Db 2 VKLVESGGGLVPRGSLKLSCAASGFTFSSYTWVWVROTPERKLEWVATISDGSSTYYP 61  
|||||  
QY 62 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSRYD---DYRDD-AMDYWGOGTTVTV 116  
|||||  
Db 62 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCTRGSGRYRDDVAMDYWGOGTTVTV 121  
|||||

QY 117 S 117  
|  
Db 122 S 122

RESULT 3  
S55536  
Ig heavy chain V region pe20 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S55536  
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A>Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin  
utations in the variable region genes.  
A:Reference number: S55528; MUID:95239763; PMID:7536850  
A:Accession: S55536  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <BOE>  
A:Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 545.5; DB 2; Length 120;  
Best Local Similarity 88.3%; Pred. No. 1.5e-41;  
Matches 106; Conservative 2; Mismatches 9; Indels 3; Gaps 1;

QY 2 VOLOESGGGLVPRGSLKLSCAASGFTFSDYYWVWVROTPERKLEWVATISDGSSTYYP 61  
|:|||||  
Db 1 VOLOESGGGLVPRGSLKLSCAASGFTFSSYTWVWVROTPERKLEWVATISDGSSTYYP 60  
|||||

QY 62 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSRYD---DAMDYWGOGTTVTVSS 118  
|||||  
Db 61 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCARLYDYDDPYMDYWGOGTTVTVSS 120  
|||||

RESULT 4  
D27889  
Ig heavy chain V region (H36-2) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C:Accession: D27889  
R:Catlon, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986  
A>Title: Structural and functional implications of a restricted antibody response to  
A:Reference number: A91043; MUID:86300658; PMID:2427335  
A:Accession: D27889  
A:Molecule type: DNA  
A:Residues: 1-119 <CAT>  
A:Experimental source: strain Balb/c  
A>Note: this sequence was determined from the germine gene  
C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.9%; Score 544; DB 2; Length 119;  
Best Local Similarity 87.4%; Pred. No. 2.1e-41;  
Matches 104; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 1 QVOLOESGGGLVPRGSLKLSCAASGFTFSDYYWVWVROTPERKLEWVATISDGSSTYYP 60  
|:|||||  
Db 1 EVOLVESGGGLVPRGSLKLSCAASGFTFSDYYWVWVROTPERKLEWVATISDGSSTYYP 60  
|||||

QY 61 PDSVKGRTISRDNKNNLYLQMSLSKSEDTAMYYCSRYD---DDAMDYWGOGTTVTVS 117  
|:|||||  
Db 61 SDYVKGRTISRDNKNNLYLQMSLSKSEDTAMYYCARDRYDDGYFDYWGAGTTVTVS 119  
|||||

RESULT 5  
S55537  
Ig heavy chain V region pe21 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S55537  
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
A>Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies u  
utations in the variable region genes.  
A:Reference number: S55528; MUID:95239763; PMID:7536850  
A:Accession: S55537  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <BOE>  
A:Cross-references: EMBL:X82590; NID:g854306; PIDN:CAA57926.1; PID:g854307  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 538.5; DB 2; Length 120;  
Best Local Similarity 87.5%; Pred. No. 6.4e-41;  
Matches 105; Conservative 2; Mismatches 10; Indels 3; Gaps 1;

QY 2 VOLOESGGGLVPRGSLKLSCAASGFTFSDYYWVWVROTPERKLEWVATISDGSSTYYP 61  
|:|||||  
Db 1 VOLOESGGGLVPRGSLKLSCAASGFTFSSYTWVWVROTPERKLEWVATISDGSSTYYP 60  
|||||

QY 62 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSRYD---DAMDYWGOGTTVTVSS 118  
|||||  
Db 61 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCTRLTYDYDDPYMDYWGOGTTVTVSS 120  
|||||

RESULT 6  
B27889  
Ig heavy chain V region (H146-24B3) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C:Accession: B27889  
R:Catlon, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A>Title: Structural and functional implications of a restricted antibody response to  
A:Reference number: A91043; MUID:86300658; PMID:2427335  
A:Accession: B27889  
A:Molecule type: DNA  
A:Residues: 1-119 <CAT>  
A:Experimental source: strain Balb/c



A:Note: this sequence was determined from the germine gene  
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin  
F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 85.0%; Score 538; DB 2; Length 119;

Best Local Similarity 87.4%; Pred. No. 7e-41; Mismatches 10; Indels 2; Gaps 1;

Matches 104; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

OY 1 OVLOESGGGLVPGGSLKSCAASGFTFSDYMWVWVROTPEKRLMVAITISDGSSTYY 60  
DB 1 EVQLVESGGGLVPGGSLKSCAASGIFTSDFYTWVWVROTPEKRLMVAITISDGSSTYY 60  
OY 61 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYD--YDDAMDYWGQGTIVTVSS 117  
DB 61 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCVRDQYDFYMDYWGQGTIVTVSS 119

## RESULT 7

S5539  
Ig heavy chain V region pe24 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S5539

R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995  
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin  
utations in the variable region genes.

A:Reference number: S55328; MUID:95239763; PMID:7536850

A:Accession: S5539

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <BOB>

A:Cross-references: EMBL:X82593; NID:9854312; PIDN:CA57929.1; PID:9854313

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:14-97/Domain: Immunoglobulin homology <IMM>

Query Match 84.4%; Score 534.5; DB 2; Length 120;

Best Local Similarity 86.7%; Pred. No. 1.4e-40;

Matches 104; Conservative 2; Mismatches 11; Indels 3; Gaps 1;

OY 2 VOLOESGGGLVPGGSLKSCAASGFTFSDYMWVWVROTPEKRLMVAITISDGSSTYY 61  
DB 1 VOLOESGGGLVPGGSLKSCAASGFTFSSYAMSVWVROTPEKRLMVAITISDGSSTYY 60  
OY 62 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYD--DAMDYWGQGTIVTVSS 118  
DB 61 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCVRDQYDFYMDYWGQGTIVTVSS 120

## RESULT 8

E27889  
Ig heavy chain V region (H158-89H4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996

C:Accession: E27888

R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a c

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: E27888

A:Molecule type: DNA

A:Residues: 1-119 <CAT>

A:Experimental source: strain Balb/c

C:Comment: This sequence was determined from the germine gene

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 84.2%; Score 533; DB 2; Length 119;

Best Local Similarity 88.1%; Pred. No. 1.9e-40;

Matches 104; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

OY 2 VOLOESGGGLVPGGSLKSCAASGFTFSDYMWVWVROTPEKRLMVAITISDGSSTYY 61  
DB 2 VKLVESGGGLVPGGSLKSCAASGFTFSSYAMSVWVROTPEKRLMVAITISDGSSTYY 61  
OY 62 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSRRR--YDDAMDYWGQGTIVTVSS 117  
DB 62 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCVRDQYDFYMDYWGQGTIVTVSS 119

## RESULT 9

S5538  
Ig heavy chain V region pe22 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S5538

R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995  
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies u  
utations in the variable region genes.

A:Reference number: S55328; MUID:95239763; PMID:7536850

A:Accession: S5538

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <BOB>

A:Cross-references: EMBL:X82591; NID:9854308; PIDN:CA57927.1; PID:9854309

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:14-97/Domain: Immunoglobulin homology <IMM>

Query Match 82.7%; Score 523.5; DB 2; Length 120;

Best Local Similarity 84.2%; Pred. No. 1.4e-39;

Matches 101; Conservative 5; Mismatches 11; Indels 3; Gaps 1;

OY 2 VOLOESGGGLVPGGSLKSCAASGFTFSDYMWVWVROTPEKRLMVAITISDGSSTYY 61  
DB 1 VKLOESGGGLVPGGSLKSCAASGFTFSSYAMSVWVROTPEKRLMVAITISDGSSTYY 60  
OY 62 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYD--DAMDYWGQGTIVTVSS 118  
DB 61 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCVRDQYDFYMDYWGQGTIVTVSS 120

## RESULT 10

E27889  
Ig heavy chain V region (H18-S415) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996

C:Accession: E27889

R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: E27889

A:Molecule type: DNA

A:Residues: 1-118 <CAT>

A:Experimental source: strain Balb/c

C:Comment: This sequence was determined from the germine gene

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:15-97/Domain: Immunoglobulin homology <IMM>

Query Match 81.8%; Score 517.5; DB 2; Length 118;

Best Local Similarity 84.0%; Pred. No. 4.6e-39;

Matches 100; Conservative 7; Mismatches 9; Indels 3; Gaps 2;

OY 1 OVLOESGGGLVPGGSLKSCAASGFTFSDYMWVWVROTPEKRLMVAITISDGSSTYY 60  
DB 1 EVQLVEFGGLVPGGSLKSCAASGIFTSDFYTWVWVROTPEKRLMVAITISDGSSTYY 60

OY 61 PDSVKGRTISRDNANKNNLYLQMSLSKSEDTAMYYCSR--YRYDDAMDYWGOGTIVTVS 117  
 |||||  
 DB 61 SOSVKGRTISRDNANKNN--YLQLSLSKSEDTAMYYCTRGSYDYDGMWGGGTSTVTS 118

## RESULT 11

I27887  
 Ig heavy chain V region (H37-45) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
 C:Accession: I27887  
 R:Calton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
 EMO J. 5, 1577-1587, 1986  
 A:Title: Structural and functional implications of a restricted antibody response to a  
 A:Reference number: A91043; MUID:86300658; PMID:2427335  
 A:Accession: I27887  
 A:Molecule type: DNA  
 A:Residues: 1-121 <CAT>  
 A:Experimental source: strain Balb/c  
 A:Note: this sequence was determined from the germline gene  
 C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 515; DB 2; Length 121;  
 Best local Similarity 83.5%; Pred. No. 7, 8e-39;  
 Matches 101; Conservative 6; Mismatches 10; Indels 4; Gaps 2;

OY 1 OVOLOESGGGLVPGGSLKSCAASGFTSDYVWVWVROTPERKLEWVATISDGSYTY 60  
 :|||  
 DB 1 EYVLVESGGGLVPGGSLKSCAASGFTFSIYAMVWRQPERKLEWVATISGGSYTY 60  
 OY 61 PDSVKGRTISRDNANKNNLYLQMSLSKSEDTAMYYCSR--YRYDD-AMDYWGOGTIVTV 116  
 |||||  
 DB 61 PDSVKGRTISRDNANKNNLYLQMSLSKSEDTAMYYCARREGLEEDYAMDYWGOGTIVTV 120  
 OY 117 S 117  
 DB 121 S 121

## RESULT 12

S55540  
 Ig heavy chain V region pe13 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 27-Oct-1995 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S55540  
 R:Boeltger, V.; Boeltger, A.; Lane, E.B.; Spruce, B.A.  
 J. Mol. Biol. 247, 932-946, 1995  
 A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin  
 A:Reference number: S55528; MUID:95239763; PMID:7536850  
 A:Accession: S55540  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-121 <BOB>  
 A:Cross-references: EMBL:X82582; NID:g854288; PIND:CA57918.1; PID:g854289  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 510; DB 2; Length 121;  
 Best local Similarity 81.8%; Pred. No. 2, 2e-38;  
 Matches 99; Conservative 6; Mismatches 12; Indels 4; Gaps 2;

OY 2 VOLOESGGGLVPGGSLKSCAASGFTSDYVWVWVROTPERKLEWVATISDGSYTY 61  
 :|||  
 DB 1 VKLOESGGGLVPGGSLKSCAASGFTFSYAMCWVRQPERKLEWVATISGGSYTY 60  
 OY 62 DSVKGRFTISRDNANKNNLYLQMSLSKSEDTAMYYCSR--YRYDD--AMDYWGOGTIVTVS 117  
 :|||  
 DB 61 DTVKGRFTISRDNANKNNLYLQMSLSKSEDTAMYYCVALYYSYDGPYAMDYWGOGTIVTVS 120

OY 118 S 118  
 DB 121 S 121

## RESULT 13

HVMS96  
 Ig heavy chain V region (6.96) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 31-Mar-1997  
 C:Accession: J70501  
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
 J. Exp. Med. 169, 2007-2019, 1989  
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar  
 A:Reference number: J70501; MUID:89279149; PMID:2499654  
 A:Accession: J70501  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-98 <LEV>  
 A:Experimental source: strain BALB/cJ  
 A:Note: this sequence belongs to the VH7183 subfamily  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:22-96/Disulfide bonds: #status predicted

Query Match 80.3%; Score 508; DB 1; Length 98;  
 Best local Similarity 96.9%; Pred. No. 2, 6e-38;  
 Matches 95; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 OVOLOESGGGLVPGGSLKSCAASGFTSDYVWVWVROTPERKLEWVATISDGSYTY 60  
 :|||  
 DB 1 EYVLVESGGGLVPGGSLKSCAASGFTSDYVWVWVROTPERKLEWVATISDGSYTY 60  
 OY 61 PDSVKGRTISRDNANKNNLYLQMSLSKSEDTAMYYCSR 98  
 |||||  
 DB 61 PDSVKGRTISRDNANKNNLYLQMSLSKSEDTAMYYCAR 98

## RESULT 14

A43413  
 Ig heavy chain V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-1996  
 C:Accession: A43413  
 R:Tomiyama, Y.; Broder, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.;  
 J. Biol. Chem. 267, 18085-18092, 1992  
 A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct speci  
 A:Reference number: A43413; MUID:92388177; PMID:1517241  
 A:Accession: A43413  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-119 <ROM>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:112815)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:9-92/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 506.5; DB 2; Length 119;  
 Best local Similarity 82.4%; Pred. No. 4, 3e-38;  
 Matches 98; Conservative 7; Mismatches 7; Indels 7; Gaps 2;

OY 7 SGGGLVPGGSLKSCAASGFTSDYVWVWVROTPERKLEWVATISDGSYTYPPSVKG 66  
 :|||  
 DB 1 SGGGLVPGGSLKSCAASGFTSDYVWVWVROTPERKLEWVATISDGSYTYHYPPSVKG 60  
 OY 67 RFTISRDNANKNNLYLQMSLSKSEDTAMYYCSR--YRYDD--AMDYWGOGTIVTVSS 118  
 :|||  
 DB 61 RFTISRDNANKNNLYLQMSLSKSEDTALYYCTRHPRFYRQCGNRYAMDYWGOGTIVTVSS 119

## RESULT 15

H27888  
 Ig heavy chain V region (H37-40) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
 C:Accession: H27888  
 R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
 EMBO J. 5, 1577-1587, 1986  
 A:Title: Structural and functional implications of a restricted antibody response to a d  
 A:Reference number: A91043; MUID:86300658; PMID:2427335  
 A:Accession: H27888  
 A:Molecule type: DNA  
 A:Residues: 1-121 <CAT>  
 A:Experimental source: strain Balb/c  
 A:Note: this sequence was determined from the germline gene  
 C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotrimer; Immunoglobulin  
 F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 79.9%; Score 506; DB 2; Length 121;  
 Best Local Similarity 80.2%; Pred. No. 4.9e-38;  
 Matches 97; Conservative 7; Mismatches 13; Indels 4; Gaps 1;  
 QY 1 QVQLQESGGGLVQPGGSLKLSCAASGFTFSIDYMYWVWVROTPPEKRLIEWVATISDGSSTYY 60  
 :||| |||||:|||| ||||| ||||| | ||||:||||| ||||| |||||  
 Db 1 EVQLVESGGGLVQPGGSLNLSCAASGFTFSYAMSWVROSPPEKRLIEWVAEISGGSSTYY 60  
 QY 61 PDSYKGRFTISRDNKNNLYLQMSLSKSEDTAMYCSR---YRYDAMDYWGQGTIVTV 116  
 :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 61 PDYVIGRFTISRDNKNTLYLEMSLSKSEDTAMYCARREGYCGSSDAMDYWGQGTIVTV 120  
 QY 117 S 117  
 :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 121 S 121

Search completed: January 13, 2003, 15:13:12  
 Job time : 15.3652 secs



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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:11:24 ; Search time 8.2087 Seconds  
(without alignments)  
278.890 Million cell updates/sec

Title: US-09-144-886-63  
Perfect score: 633  
Sequence: 1 QVQLQESGGGLVFRGGSGLK.....YRVDAMDYWGCGTTVYSS 118

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues  
Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEM\_PUB pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCRT\_NEM\_PUB pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEM\_PUB pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEM\_PUB pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/PCRTUS\_PUBCOMB pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEM\_PUB pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEM\_PUB pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEM\_PUB pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	633	100.0	118	US-09-144-886-63	Sequence 63, Appl
2	597	94.3	118	US-09-144-886-63	Sequence 62, Appl
3	522	84.5	118	US-09-144-886-65	Sequence 65, Appl
4	519	84.0	118	US-09-144-886-63	Sequence 64, Appl
5	518	81.9	144	US-09-881-823-12	Sequence 12, Appl
6	511	80.8	123	US-09-144-886-60	Sequence 60, Appl
7	507	80.2	140	US-09-286-240-4	Sequence 4, Appl
8	504	79.6	118	US-09-144-886-67	Sequence 67, Appl
9	503	79.5	118	US-09-144-886-66	Sequence 66, Appl
10	501	79.1	118	US-09-423-800-46	Sequence 46, Appl
11	501	79.1	137	US-09-423-800-76	Sequence 76, Appl
12	493.5	78.0	140	US-10-006-773-4	Sequence 4, Appl
13	484.5	76.5	269	US-10-027-770-5	Sequence 5, Appl
14	475.5	75.1	120	US-10-027-770-2	Sequence 2, Appl
15	474	74.9	120	US-08-229-200A-6	Sequence 6, Appl
16	473	74.7	443	US-09-917-410-4	Sequence 4, Appl
17	472.5	74.6	119	US-09-736-371B-17	Sequence 17, Appl
18	472.5	74.6	119	US-10-060-714-17	Sequence 17, Appl
19	469	74.1	118	US-09-423-800-56	Sequence 56, Appl

20	469	74.1	137	US-09-423-800-77	Sequence 77, Appl
21	468.5	74.0	123	US-09-144-886-61	Sequence 61, Appl
22	466.5	73.7	245	US-09-956-086-5	Sequence 5, Appl
23	466.5	73.7	245	US-09-956-087-5	Sequence 5, Appl
24	466	73.6	98	US-09-840-459-39	Sequence 39, Appl
25	465.5	73.5	265	US-09-985-442-5	Sequence 5, Appl
26	465.5	73.5	265	US-09-983-580-5	Sequence 5, Appl
27	464	73.3	98	US-09-840-459-38	Sequence 38, Appl
28	462	73.0	98	US-09-840-459-45	Sequence 45, Appl
29	460.5	72.7	117	US-08-790-540A-6	Sequence 6, Appl
30	460.5	72.7	117	US-08-791-391A-6	Sequence 6, Appl
31	460	72.7	120	US-10-025-687-4	Sequence 4, Appl
32	459.5	72.6	449	US-09-736-371B-21	Sequence 21, Appl
33	457	72.2	98	US-09-840-459-41	Sequence 41, Appl
34	455	71.9	120	US-09-810-502-34	Sequence 34, Appl
35	455	71.9	133	US-10-006-773-9	Sequence 9, Appl
36	454	71.7	98	US-09-840-459-44	Sequence 44, Appl
37	454	71.7	120	US-09-229-200A-25	Sequence 25, Appl
38	453.5	71.6	117	US-09-840-459-83	Sequence 83, Appl
39	453	71.6	120	US-09-229-200A-28	Sequence 28, Appl
40	451.5	71.3	119	US-09-811-123-3	Sequence 3, Appl
41	451.5	71.3	138	US-09-736-744-15	Sequence 15, Appl
42	448.5	70.9	125	US-09-840-459-76	Sequence 76, Appl
43	448	70.8	128	US-09-840-459-77	Sequence 77, Appl
44	448	70.8	128	US-09-840-459-79	Sequence 79, Appl
45	448	70.8	263	US-09-956-086-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-09-144-886-63  
; Sequence 63, Application US/09144886  
; Patent No. US2002015114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; TITLE OF INVENTION: Botulinum Neurotoxins  
; FILE REFERENCE: 2500.117USO  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 63  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
; OTHER INFORMATION: C25 region VH epitope 2  
US-09-144-886-63

Query Match 100.0% Score 633; DB 9; Length 118;  
Best Local Similarity 100.0%; Pred. No. 1.1e-42;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGGGLVFRGGSGLKSCAASGFTSDYMYWVWVROTPEKRLKLVATISDGSYTY 60  
DB 1 QVQLQESGGGLVFRGGSGLKSCAASGFTSDYMYWVWVROTPEKRLKLVATISDGSYTY 60

QY 61 PSVKGRTFTSRDNNKNNLYLQSSLSKSEDTAMYSRTRYDDAMDYWGCGTTVYSS 118  
DB 61 PSVKGRTFTSRDNNKNNLYLQSSLSKSEDTAMYSRTRYDDAMDYWGCGTTVYSS 118

RESULT 2  
US-09-144-886-62  
; Sequence 62, Application US/09144886  
; Patent No. US2002015114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D

APPLICANT: Amersdorfer, Peter  
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
FILE REFERENCE: 2500.117USO  
CURRENT APPLICATION NUMBER: US/09/144,886  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: PatentIn Ver. 2.0  
LENGTH: 118  
TYPE: PR1  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-62

Query Match 94.3%; Score 597; DB 9; Length 118;  
Best Local Similarity 94.1%; Pred. No. 6.3e-40;  
Matches 111; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVOLOESGGGLVPRGSLKLSKSCAASGFTFSDYMWYWRQTPERKLEWVATISDGGSTYY 60  
Db 1 EVKLVESSGGGLVPRGSLKLSKSCAASGFTFSDYMSWVRQTPERKLEWVATISDGGSTYY 60  
QY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRYRYDDAMDYWGCGTIVTVSS 118  
Db 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAITYCYRYRDEBDLDYWGCGTIVTVSS 118

RESULT 3  
US-09-144-886-65  
Sequence 65, Application US/09144886  
Patent No. US20020155114A1  
GENERAL INFORMATION:  
APPLICANT: Marks, James D  
APPLICANT: Amersdorfer, Peter  
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
FILE REFERENCE: 2500.117USO  
CURRENT APPLICATION NUMBER: US/09/144,886  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: PatentIn Ver. 2.0  
LENGTH: 118  
TYPE: PR1  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-65

Query Match 82.5%; Score 522; DB 9; Length 118;  
Best Local Similarity 83.9%; Pred. No. 3.8e-34;  
Matches 99; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVOLOESGGGLVPRGSLKLSKSCAASGFTFSDYMWYWRQTPERKLEWVATISDGGSTYY 60  
Db 1 EVKLVESSGGGLVPRGSLKLSKSCAASGFTFSSYMSWVRQTPERKLEWVATISDGGSTYY 60  
QY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRYRYDDAMDYWGCGTIVTVSS 118  
Db 61 TDVWKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCARNLPHYHDVWVGCGTIVTVSS 118

RESULT 4  
US-09-144-886-64  
Sequence 64, Application US/09144886  
Patent No. US20020155114A1  
GENERAL INFORMATION:  
APPLICANT: Marks, James D  
APPLICANT: Amersdorfer, Peter

TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
FILE REFERENCE: 2500.117USO  
CURRENT APPLICATION NUMBER: US/09/144,886  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: PatentIn Ver. 2.0  
LENGTH: 118  
TYPE: PR1  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-64

Query Match 82.0%; Score 519; DB 9; Length 118;  
Best Local Similarity 83.9%; Pred. No. 6.5e-34;  
Matches 99; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVOLOESGGGLVPRGSLKLSKSCAASGFTFSDYMWYWRQTPERKLEWVATISDGGSTYY 60  
Db 1 EVKLVESSGGGLVPRGSLKLSKSCAASGFTFSSYMSWVRQTPERKLEWVATISDGGSTYY 60  
QY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRYRYDDAMDYWGCGTIVTVSS 118  
Db 61 TDVWKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCARNLPHYHDVWVGCGTIVTVSS 118

RESULT 5  
US-09-881-823-12  
Sequence 12, Application US/09881823  
Patent No. US20020068066A1  
GENERAL INFORMATION:  
APPLICANT: SHI, WENYUAN  
APPLICANT: ANDERSON, MAXWELL  
APPLICANT: MORRISON, SHERIE  
APPLICANT: TRINH, RYAN  
APPLICANT: WIMS, LETITIA  
APPLICANT: CHEN, LI  
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries  
FILE REFERENCE: 22851-032  
CURRENT APPLICATION NUMBER: US/09/881,823  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: US 07/378,577  
PRIOR FILING DATE: 1999-08-20  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.0  
LENGTH: 144  
TYPE: PR1  
ORGANISM: Murine  
US-09-881-823-12

Query Match 81.9%; Score 518.5; DB 10; Length 144;  
Best Local Similarity 82.3%; Pred. No. 8.5e-34;  
Matches 102; Conservative 5; Mismatches 8; Indels 9; Gaps 2;

QY 2 VQLOESGGGLVPRGSLKLSKSCAASGFTFSDYMWYWRQTPERKLEWVATISDGGSTYY 61  
Db 21 VKLVESGGGLVPRGSLKLSKSCAASGFTFSSYMSWVRQTPERKLEWVATISDGGSTYY 80  
QY 62 DSVKGRFTTISRDNKNNLYLQMSLSKSEDTAMYYCSR-----YRDDAMDYWGCGTIV 114  
Db 81 DSVKGRFTTISRDNKNNLYLQMSLSKSEDTAMYYCSRSDGSGSYTY--AMDYWGCGTSV 138

QY 115 TVSS 118  
Db 139 TVSS 142  
RESULT 6  
US-09-144-886-60

; Sequence 60, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; FILE REFERENCE: 2500.117USO  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 60  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
; OTHER INFORMATION: 1A1 region VH epitope 2  
US-09-144-886-60

Query Match 80.8%; Score 511.5; DB 9; Length 123;  
Best Local Similarity 78.9%; Pred. No. 2.6e-33;  
Matches 97; Conservative 9; Mismatches 12; Indels 5; Gaps 1;

OY 1 OVQLOESGGGLVKGPGSLKLSGASGFTFSDYMWVWVROTPKRLKLEWATISDGGSTYY 60

DB 1 EVKLVESSGGGLVKGPGSLKLSGASGFTFSDYMWVWVROTPKRLKLEWATISDGGSTYY 60

OY 61 PDSVAGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYRD-----AMDYWGQGTYY 115

DB 61 PDSVAGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYRD-----AMDYWGQGTYY 120

OY 116 VSS 118  
DB 121 VSS 123

## RESULT 7

; Sequence 4, Application US/09286240  
; Patent No. US20020010320A1  
; GENERAL INFORMATION:  
; APPLICANT: Felt; James W  
; TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin  
; FILE REFERENCE: 110498/74073  
; CURRENT APPLICATION NUMBER: US/09/286,240  
; CURRENT FILING DATE: 1999-04-05  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-286-240-4

Query Match 80.2%; Score 507.5; DB 10; Length 140;  
Best Local Similarity 81.8%; Pred. No. 5.8e-33;  
Matches 99; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

OY 1 OVQLOESGGGLVKGPGSLKLSGASGFTFSDYMWVWVROTPKRLKLEWATISDGGSTYY 60

DB 20 EVMLVESGGGLVKGPGSLKLSGASGFTFSSYTWVWVROTPKRLKLEWATISDGGSTYY 79

OY 61 PDSVAGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSR---YRDDAMDYWGQGTYY 117

DB 80 PDSVAGRTTISRDNKNNLYLQMSLSKSEDTALYYCTRIGDYGAVTMDYWGQGTYY 139

OY 118 S 118  
DB 140 S 140

RESULT 8  
US-09-144-886-67

; Sequence 67, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; FILE REFERENCE: 2500.117USO  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 67  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
; OTHER INFORMATION: 3H4 region VH epitope 2  
US-09-144-886-67

Query Match 79.6%; Score 504; DB 9; Length 118;  
Best Local Similarity 81.4%; Pred. No. 9.3e-33;  
Matches 96; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

OY 1 OVQLOESGGGLVKGPGSLKLSGASGFTFSDYMWVWVROTPKRLKLEWATISDGGSTYY 60

DB 1 EVKLVESSGGGLVKGPGSLKLSGASGFTFSSYTWVWVROTPKRLKLEWATISDGGSTYY 60

OY 61 PDSVAGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYRDAMDYWGQGTYY 118

DB 61 TDVVGRTTISRDNKNNLYLQMSLSKSEDTAMYYCARNLPHYDHYWGQGTYY 118

## RESULT 9

; Sequence 66, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; FILE REFERENCE: 2500.117USO  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 66  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
; OTHER INFORMATION: 3F4 region VH epitope 2  
US-09-144-886-66

Query Match 79.5%; Score 503; DB 9; Length 118;  
Best Local Similarity 82.8%; Pred. No. 1.1e-32;  
Matches 96; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 3 QLOESGGGLVKGPGSLKLSGASGFTFSDYMWVWVROTPKRLKLEWATISDGGSTYY 62

DB 3 KLVESSGGGLVKGPGSLKLSGASGFTFSSYTWVWVROTPKRLKLEWATISDGGSTYY 62

OY 63 SVKGRFTTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYRDDAMDYWGQGTYY 118

DB 63 NVKGRFTTISRDNKNNLYLQMSLSKSEDTAMYYCARNLPHYDHYWGQGTYY 118

## RESULT 10

US-09-423-800-46  
; Sequence 46, Application US/09423800  
; Patent No. US20020165363A1  
; GENERAL INFORMATION:  
; APPLICANT: SATO, KOH  
; APPLICANT: TSUNENARI, TOSHIAKI  
; APPLICANT: ISHII, KIMIE  
; TITLE OF INVENTION: CACHEXIA REMEDY  
; FILE REFERENCE: 04853-0036  
; CURRENT APPLICATION NUMBER: US/09/423, 800  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: PCT/JP98/02116  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: JP 125505/1997  
; PRIOR FILING DATE: 1997-05-15  
; PRIOR APPLICATION NUMBER: JP 194445/1997  
; PRIOR FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-423-800-46

Query Match 79.1%; Score 501; DB 9; Length 118;  
Best Local Similarity 81.4%; Pred. No. 1.6e-32;  
Matches 96; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVLOESGGGLVPGGSLKSCAASGFTSDYYWVWVROTPEKRLLEVAVATISDGGSTYY 60  
DB 1 EVLVESGGGLVPGGSLKSCAASGFTSSYGMWIRQTPDKRLEWVATISSGGSTYY 60  
QY 61 PDSVKGFTISRDNANKNTLYLQMSLSKSEDTAMFYCSRYYDDAMDYWGCTVTYVS 118  
DB 61 PDSVKGFTISRDNANKNTLYLQMSLSKSEDTAMFYCARQTTMTYFAYWGGTLVTYSA 118

RESULT 11  
US-09-423-800-76  
; Sequence 76, Application US/09423800  
; Patent No. US20020165363A1  
; GENERAL INFORMATION:  
; APPLICANT: SATO, KOH  
; APPLICANT: TSUNENARI, TOSHIAKI  
; APPLICANT: ISHII, KIMIE  
; TITLE OF INVENTION: CACHEXIA REMEDY  
; FILE REFERENCE: 04853-0036  
; CURRENT APPLICATION NUMBER: US/09/423, 800  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: PCT/JP98/02116  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: JP 125505/1997  
; PRIOR FILING DATE: 1997-05-15  
; PRIOR APPLICATION NUMBER: JP 194445/1997  
; PRIOR FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 76  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-423-800-76

Query Match 79.1%; Score 501; DB 9; Length 137;  
Best Local Similarity 81.4%; Pred. No. 1.8e-32;  
Matches 96; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVLOESGGGLVPGGSLKSCAASGFTSDYYWVWVROTPEKRLLEVAVATISDGGSTYY 60  
DB 20 EVLVESGGGLVPGGSLKSCAASGFTSSYGMWIRQTPDKRLEWVATISSGGSTYY 79  
QY 61 PDSVKGFTISRDNANKNTLYLQMSLSKSEDTAMFYCSRYYDDAMDYWGCTVTYVS 118

DB 80 PDSVKGFTISRDNANKNTLYLQMSLSKSEDTAMFYCARQTTMTYFAYWGGTLVTYSA 137  
RESULT 12  
US-10-006-773-4  
; Sequence 4, Application US/10006773  
; Patent No. US20020132983A1  
; GENERAL INFORMATION:  
; APPLICANT: Jungheun, Richard P.  
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor A  
; FILE REFERENCE: 003  
; CURRENT APPLICATION NUMBER: US/10/006, 773  
; CURRENT FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 60/250, 089  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patentln version 3.1  
; SEQ ID NO 4  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-006-773-4

Query Match 78.0%; Score 493.5; DB 12; Length 140;  
Best Local Similarity 79.3%; Pred. No. 7e-32;  
Matches 96; Conservative 7; Mismatches 15; Indels 3; Gaps 1;

QY 1 QVLOESGGGLVPGGSLKSCAASGFTSDYYWVWVROTPEKRLLEVAVATISDGGSTYY 60  
DB 20 EVLVESGGGLVPGGSLKSCAASGFTSRYAMSVWVROTPEKRLLEVAVATISSGGSTYY 79  
QY 61 PDSVKGFTISRDNANKNTLYLQMSLSKSEDTAMFYCSRYYDDA---MDYWGCTVTYVS 117  
DB 80 PDSVKGFTISRDNANKNTLYLQMSLSKSEDTALTYCARQYDGCANFEDYWGCTVTYVS 139  
QY 118 S 118  
DB 140 S 140

RESULT 13  
US-10-027-770-5  
; Sequence 5, Application US/10027770  
; Patent No. US20020151684A1  
; GENERAL INFORMATION:  
; APPLICANT: MATER, BRUCE  
; APPLICANT: SARSELA, KALLE  
; APPLICANT: KIRCHAUSEN, TOMAS  
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF  
; FILE REFERENCE: 701039-050001-C  
; CURRENT APPLICATION NUMBER: US/10/027, 770  
; CURRENT FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: PCT/US00/17929  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: 60/141, 896  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a  
; OTHER INFORMATION: second-generation ScFv derived from monoclonal  
; OTHER INFORMATION: antibody 9E10 with site directed mutagenesis  
US-10-027-770-5

Query Match 76.5%; Score 484.5; DB 12; Length 269;  
Best Local Similarity 75.6%; Pred. No. 6.3e-31;  
Matches 96; Conservative 9; Mismatches 13; Indels 9; Gaps 2;



QY 1 QVQLQESGGSGLVKRRGSGSLTKLTSCAASGCTFSPSYVYVAVRQPKRLKEVAWATISGGSTYY 60

Db 6 EVKLVEGSGDLVYKRGSGSLTKLTSCAASGCTFSPHYGSMVVRQTPDKRLKEVAWATISGSGTTHY 65

QY 61 PDSYKSGFFETISRQAKNNLTLQWLSLSEPTAWYCSR----RYSD-----AMDYGGG 111

Db 66 PDSYKSGFFETISRDNDKALTLQNNLSLSEDTAWYICARNSSEFYIYGNVYYSAADTWGG 125

QY 112 TTYTVSS 118 |

Db 126 ASYTVSS 132

RESULT 14  
 US-10-027-770-2  
 : Sequence 2, Application US/10027770  
 : Patent No. US20020151684A1  
 : GENERAL INFORMATION:  
 : APPLICANT: MAYER, BRUCE  
 : APPLICANT: SAKSELA, KALLE  
 : APPLICANT: KIRCHAUSEN, TOMAS  
 : TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF  
 : FILE REFERENCE: /701039-050001-C  
 : CURRENT APPLICATION NUMBER: US/10/027,770  
 : PRIORITY FILING DATE: 2002-06-13  
 : PRIOR APPLICATION NUMBER: PCT/US00/17929  
 : PRIORITY FILING DATE: 2000-06-29  
 : PRIOR APPLICATION NUMBER: 60/141,896  
 : PRIOR FILING DATE: 1999-06-30  
 : NUMBER OF SEQ ID NOS: 5  
 : SOFTWARE: PatentIn Ver. 2.1  
 : SEQ ID NO 2  
 : LENGTH: 269  
 : TYPE: PRT  
 : ORGANISM: Unknown Organism  
 : FEATURE:  
 : OTHER INFORMATION: Description of Unknown Organism: 3DX, a  
 : OTHER INFORMATION: second generation ScFv derived from monoclonal  
 : OTHER INFORMATION: antibody 9E10  
 : US-10-027-770-2

[illegible]

RESULT 15  
US-09-229-200A-6  
Sequence 6, Application US/09229200A  
Patent No. US20020099179A1  
GENERAL INFORMATION:  
APPLICANT: Jolliffe et al.  
TITLE OF INVENTION: CD4 Specific Recombinant Antibody  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Johnson & Johnson  
STREET: One Johnson & Johnson Plaza  
CITY: New Brunswick  
STATE: NJ  
COUNTRY: USA  
ZIP: 08933-7003

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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: <unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229, 200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: John W. Mallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORI-948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 784-3239
TELEFAX: (908) 524-2808
INFORMATION FOR SEQ. ID NO. 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 120
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-229-200A-6
4

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[illegible]

Search completed: January 13, 2003, 15:14:04  
Job time : 9.2087 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2003, 15:10:24 : Search time 11.8 Seconds  
(without alignments) 294.229 Million cell updates/sec

Title: US-09-144-886-63

Perfect score: 633

Sequence: 1 OVOLOESGGGLVKGSLK.....YRYDAMDYWGQTTTVSS 118

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*

2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*

3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*

4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*

5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*

6: /cgn2\_6/ptodata/1/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575.5	90.9	123	4	US-09-344-587-13
2	532	84.0	159	2	US-08-653-402B-2
3	522.5	82.5	217	5	PCT-US94-14106-59
4	510.5	80.6	239	2	US-08-553-497A-18
5	504	79.6	118	5	PCT-US93-08435-10
6	503.5	79.5	137	1	US-08-331-398A-61
7	503.5	79.5	137	2	US-08-331-397B-61
8	503.5	79.5	137	2	US-08-759-804A-60
9	502	79.3	123	1	US-08-356-272-3
10	499.5	78.9	125	1	US-08-331-398A-65
11	499.5	78.9	125	2	US-08-331-397B-65
12	499.5	78.9	125	2	US-08-759-804A-64
13	499	78.8	135	4	US-08-579-378A-16
14	497	78.5	300	2	US-08-661-052-4
15	497	78.5	300	4	US-09-188-082-4
16	497	78.5	300	4	US-09-364-088-4
17	497	78.5	300	4	US-09-102-716-4
18	496	78.4	118	1	US-08-326-362-2
19	494	78.0	301	2	US-08-661-052-14
20	494	78.0	301	4	US-09-188-082-14
21	494	78.0	301	4	US-09-364-088-14
22	494	78.0	301	4	US-09-102-716-14
23	494	78.0	553	2	US-08-661-052-16
24	494	78.0	553	4	US-09-188-082-16
25	494	78.0	553	4	US-09-364-088-16
26	494	78.0	553	4	US-09-102-716-16
27	493.5	78.0	113	1	US-07-789-344A-10

28	492.5	77.8	239	2	US-07-956-399-4	Sequence 4, Appl1
29	491.5	77.6	138	2	US-08-379-057-14	Sequence 14, Appl1
30	490.5	77.5	158	2	US-08-653-402B-6	Sequence 6, Appl1
31	490.5	77.5	158	2	US-08-653-402B-10	Sequence 10, Appl1
32	486.5	76.9	109	2	US-08-793-490-6	Sequence 6, Appl1
33	485	76.6	122	5	PCT-US93-08435-12	Sequence 12, Appl1
34	485	76.6	122	5	PCT-US93-08435-43	Sequence 43, Appl1
35	484.5	76.5	119	1	US-08-285-936-6	Sequence 6, Appl1
36	484.5	76.5	119	1	US-08-487-860-6	Sequence 6, Appl1
37	483.5	76.4	119	1	US-08-285-936-2	Sequence 2, Appl1
38	483.5	76.4	119	1	US-08-487-860-2	Sequence 2, Appl1
39	483	76.3	247	6	5455030-9	Sequence 14, Appl1
40	482.5	76.2	447	5	5455030-1	Sequence 23, Appl1
41	482	76.1	122	5	PCT-US93-08435-14	Sequence 12, Appl1
42	478.5	75.6	140	3	US-08-836-561-23	Sequence 12, Appl1
43	477.5	75.4	119	1	US-08-285-936-12	Sequence 12, Appl1
44	477.5	75.4	119	1	US-08-487-860-12	Sequence 12, Appl1
45	477.5	75.4	119	2	US-08-475-000-16	Sequence 16, Appl1

## ALIGNMENTS

RESULT 1

US-09-344-587-13

Sequence 13, Application US/09344587

Patent No. 6331402

GENERAL INFORMATION:

APPLICANT: Praast, Gerald

APPLICANT: Nussbaum, Sabine

APPLICANT: Moessner, Ellen

APPLICANT: Lenz, Helmut

TITLE OF INVENTION: REDUCTION OF INTERFERENCE OF IMMUNOSSAYS BY SUBSTANCES

TITLE OF INVENTION: DERIVED FROM THE FRAMEWORK REGIONS OF ANTIBODIES

FILE REFERENCE: BMID 9928 4897/00/US-Im

CURRENT APPLICATION NUMBER: US/09/344,587

CURRENT FILING DATE: 1999-06-25

EARLIER APPLICATION NUMBER: DE 19828466.7

EARLIER FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 123

TYPE: PRT

ORGANISM: Mus musculus

US-09-344-587-13

Query Match

Best Local Similarity 90.9%; Score 575.5; DB 4; Length 123;

Matches 110; Conservative 4; Mismatches 4; Indels 5; Gaps 1;

QY 1 OVOLOESGGGLVKGSLKSCAASGFTFSDYYWVROTPEKRLKLVATISDGSSTYY 60

1 EVQGVESGGGLVKGSLKSCAASGFTFSDYYWVROTPEKRLKLVATISDGSSTYY 60

QY 61 PSVKGRTFISDNKNNLYLWSSLSKSDTAMVYCSRR-----DDAMDYWGQTTTVT 115

61 PSVKGRTFISDNKNNLYLWSSLSKSDTAMVYCSRR-----DDAMDYWGQTTTVT 120

DB 61 PSVKGRTFISDNKNNLYLWSSLSKSDTAMVYCSRR-----DDAMDYWGQTTTVT 120

QY 116 VSS 118

111

DB 121 VSS 123

RESULT 2

US-08-653-402B-2

Sequence 2, Application US/08653402B

Patent No. 5969107

GENERAL INFORMATION:

APPLICANT: CARCELLER, Ana

APPLICANT: ROSELLI, Elisabet

APPLICANT: GOMEZ, Alicia

APPLICANT: ADEN, Jaume

APPLICANT: PILATS, Jaume  
TITLE OF INVENTION: Anti-Idiotypic antibodies which induce an  
TITLE OF INVENTION: Immune response against epidermal growth factor receptor.  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.  
STREET: 2200 Clarendon Boulevard, Suite 1400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/653,402B  
FILING DATE: 24-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95107967.2  
FILING DATE: 26-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lebovitz, Richard M.  
REGISTRATION NUMBER: 37,067  
REFERENCE/DOCKET NUMBER: MERCK 1781  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 159 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-653-402B-2

Query Match 84.0%; Score 532; DB 2; Length 159;  
Best Local Similarity 80.5%; Pred. No. 4.3e-46;  
Matches 103; Conservative 6; Mismatches 7; Indels 12; Gaps 2;

QY 1 QVLOESGGGLVPRGSGSLKSCAASGFTSDYVWVWRQTPERKLEWVATISDGSYTY 60  
:|||||  
DB 20 EVQLVESGGGLVPRGSGSLKSCAASGFTSDYVWVWRQHPGRKLEWVATISDGYTY 79  
:|||||  
QY 61 PDVSKGRFTISRDNKANKNLVLOMSLSKSEPTAMYYCSR-----YKRDAMDYWGQ 110  
:|||||  
DB 80 PDVSKGRFTISRDNKANKNLVLOMSLSKSEPTAMVFCARDGAARTSSQVYY--GMDYWGQ 137  
:|||||  
QY 111 GTVTWSS 118  
:|||||  
DB 138 GTVTWSS 145

RESULT 3  
PCT-US94-14106-59  
Sequence 59, Application PC/TUS9414106  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Process for Generating Specific Antibodies  
NUMBER OF SEQUENCES: 61  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/14106  
FILING DATE:  
CLASSIFICATION:  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:

LENGTH: 217 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-14106-59

Query Match 82.5%; Score 522.5; DB 5; Length 217;  
Best Local Similarity 84.7%; Pred. No. 5.4e-45;  
Matches 100; Conservative 6; Mismatches 9; Indels 3; Gaps 1;

QY 1 QVLOESGGGLVPRGSGSLKSCAASGFTSDYVWVWRQTPERKLEWVATISDGSYTY 60  
:|||||  
DB 1 EVQLVESGGGLVPRGSGSLKSCAASGFTSDYVWVWRQTPERKLEWVATISDGYTY 60  
:|||||  
QY 61 PDVSKGRFTISRDNKANKNLVLOMSLSKSEPTAMYYCSRYRDAMDYWGQGTWVSS 118  
:|||||  
DB 61 ADVSKGRFTISRDNKANKNLVLOMSLSKSEPTAMVYCAR---DPLVSGMGGTITWSS 115  
:|||||

RESULT 4  
US-08-553-497A-18  
Sequence 18, Application US/08553497A  
Patent No. 5844093  
GENERAL INFORMATION:  
APPLICANT: KETTERBOURGH, C. A.  
APPLICANT: BENDIG, MARY M.  
APPLICANT: ANSELL, KEITH H.  
APPLICANT: GUSSON, DETLEF  
APPLICANT: ADAM, JAUME  
APPLICANT: MITJANS, FRANCESCA  
APPLICANT: ROSELL, ELISABET  
APPLICANT: BLASCO, FRANCESC  
APPLICANT: PILATS, JAUME  
TITLE OF INVENTION: ANTI-BEGR SINGLE-CHAIN FVS AND ANTI-BEGR  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD. SUITE 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,497A  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/00978  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94104160.0  
FILING DATE: 17-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94118970.6  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1726  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-553-497A-18

Query Match 80.6%; Score 510.5; DB 2; Length 239;  
Best Local Similarity 84.0%; Pred. No. 9,6e-44;  
Matches 100; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

OY 1 OVOLQESGGGLVKGSGSLKLSGASGFTFSDYYWVWVROTPEKRLKLEWVATISDGGSTYY 60  
DB 1 EVKLDESGLDLVPGGSLKLSGASGFTFSSYGSWVROTPEKRLKLEWVATISGGAITY 60  
OY 61 PDVVGKRFITSRDNKNNLYLQMSLSKSEDTAMYYCSRYYDD-AMDYWGCGTIVYSS 118  
DB 61 PSVVGKRFITSRDNKNNLYLQMSLSKSEDTAMYYCARLETGDXALDYWGCGTIVYSS 119

RESULT 5  
PCT-US93-08435-10

Sequence 10, Application PC/TUS9308435

GENERAL INFORMATION:

APPLICANT: SmithKline Beecham Corporation

APPLICANT: U.S. Government, Secretary of

APPLICANT: the Navy

APPLICANT: U.S. Government, Secretary of

APPLICANT: the Army

TITLE OF INVENTION: Monoclonal Antibodies for Confering Passive

TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESS: Howson and Howson

STREET: Box 457, 321 Norristown Road

CITY: Spring House

STATE: PA

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08435

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/941,654

FILING DATE: 09-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: SBC P50107

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 540-9200

TELEFAX: (215) 540-5818

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US93-08435-10

Query Match 79.6%; Score 504; DB 5; Length 118;  
Best Local Similarity 82.9%; Pred. No. 1.9e-43;  
Matches 97; Conservative 7; Mismatches 9; Indels 4; Gaps 2;

OY 6 EESGGGLVKGSGSLKLSGASGFTFSDYYWVWVROTPEKRLKLEWVATISDGGSTYY 65  
DB 2 EESGGGLVKGSGSLKLSGASGFTFSSYGSWVROTPEKRLKLEWVATISDGGSTYY 61  
OY 66 GFTTISRDNKNNLYLQMSLSKSEDTAMYYCSR--YRYDD-AMDYWGCGTIVYSS 118  
DB 62 GFTTISRDNKNNLYLQMSLSKSEDTAMYYCASLIYGYDGYAMDYWGCGTIVYSS 118

RESULT 6  
US-08-331-398A-61

Sequence 61, Application US/08331398A

Patent No. 5608039

GENERAL INFORMATION:

APPLICANT: Pastan, Ira

APPLICANT: Willingham, Mark

APPLICANT: Fitzgerald, David

APPLICANT: Brinkmann, Ulrich

APPLICANT: Pal, Lee

TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins

TITLE OF INVENTION: and Their Uses (as amended)

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Crew

STREET: One Market Plaza, Stewart Street Plaza

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/331,398A

FILING DATE: 28-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/767,331

FILING DATE: 30-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/596,289

FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 015280-126110US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 137 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Region

LOCATION: 1..137

OTHER INFORMATION:

OTHER INFORMATION: /note="Mouse monoclonal antibody B1 Fv

US-08-331-398A-61

Query Match 79.5%; Score 503.5; DB 1; Length 137;  
Best Local Similarity 82.6%; Pred. No. 2.5e-43;  
Matches 100; Conservative 4; Mismatches 14; Indels 3; Gaps 2;

OY 1 OVOLQESGGGLVKGSGSLKLSGASGFTFSDYYWVWVROTPEKRLKLEWVATISDGGSTYY 60  
DB 1 EVKLDESGLDLVPGGSLKLSGASGFTFSDNYWVWVROTPEKRLKLEWVATISDGGSTYY 60  
OY 61 PDVVGKRFITSRDNKNNLYLQMSLSKSEDTAMYYCSR--YRYDDA-MDYWGCGTIVYSS 117  
DB 61 PSVVGKRFITSRDNKNNLYLQMSLSKSEDTAMYYCGRSPYDYDAPFTYWGCGTIVYSS 120  
OY 118 S 118  
DB 121 A 121

## RESULT 7

US-08-331-397B-61

; Sequence 61, Application US/08331397B

; Patent No. 5981726

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira

; APPLICANT: Benhar, Itai

; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-

; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses

; NUMBER OF SEQUENCES: 68

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One Market Plaza, Stewart Street Plaza

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105-1492

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/331,397B

; FILING DATE: 28-OCT-1994

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 07/767,331

; FILING DATE: 30-SEP-1991

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 07/596,289

; FILING DATE: 12-OCT-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Hunter, Tom

; REGISTRATION NUMBER: 38,498

; REFERENCE/DOCKET NUMBER: 015280-126120US

; TELEPHONE: (415) 543-9600

; TELEFAX: (415) 543-5043

; INFORMATION FOR SEQ ID NO: 61:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 137 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Region

; LOCATION: 1..137

; OTHER INFORMATION: /note="Mouse monoclonal antibody B1 Fv

; OTHER INFORMATION: Heavy chain region"

; US-08-331-397B-61

Query Match 79.5%; Score 503.5; DB 2; Length 137;  
Best Local Similarity 82.6%; Pred. No. 2.5e-43;  
Matches 100; Conservative 4; Mismatches 14; Indels 3; Gaps 2;

QY 1 QVQLQESGGGLVPGGSLKSCAASGFTPSDYMYWVWVROTPEKRLKLVAVATISDGGSYTY 60  
:|||||  
DB 1 EVQLVDSGGGLVPGGSLKSCAASGFTPSDNYMYWVWVROTPEKRLKLVAVATISDGGTYIDY 60  
QY 61 PDSVKGRTISRDNKNNLYLQSSLSKSEDTAMYYCSR--YRDDA-MDYWGCGTIVTVS 117  
:|||||  
DB 61 SDSVKGRFTISRDNKNNLYLQSSLSRSEDTGMYYGRSPYYDYVAFPTWGGGTIVTVS 120  
QY 118 S 118  
DB 121 A 121

## RESULT 8

US-08-759-804A-60

; Sequence 60, Application US/08759804A

; Patent No. 5990296

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira

; APPLICANT: Willingham, Mark

; APPLICANT: Fitzgerald, David J.

; APPLICANT: Brinkmann, Ulrich

; APPLICANT: Pai, Lee

; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,

; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof

; NUMBER OF SEQUENCES: 68

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/759,804A

; FILING DATE: 03-DEC-1996

; CLASSIFICATION: 536

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/331,398

; FILING DATE: 28-OCT-1994

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 07/767,331

; FILING DATE: 30-SEP-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen L.

; REGISTRATION NUMBER: 32,762

; REFERENCE/DOCKET NUMBER: 015280-126140US

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 60:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 137 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Region

; LOCATION: 1..137

; OTHER INFORMATION: /note="Mouse monoclonal antibody B1 Fv

; OTHER INFORMATION: Heavy chain region"

; US-08-759-804A-60

Query Match 79.5%; Score 503.5; DB 2; Length 137;  
Best Local Similarity 82.6%; Pred. No. 2.5e-43;  
Matches 100; Conservative 4; Mismatches 14; Indels 3; Gaps 2;

QY 1 QVQLQESGGGLVPGGSLKSCAASGFTPSDYMYWVWVROTPEKRLKLVAVATISDGGSYTY 60  
:|||||  
DB 1 EVQLVDSGGGLVPGGSLKSCAASGFTPSDNYMYWVWVROTPEKRLKLVAVATISDGGTYIDY 60  
QY 61 PDSVKGRTISRDNKNNLYLQSSLSKSEDTAMYYCSR--YRDDA-MDYWGCGTIVTVS 117  
:|||||  
DB 61 SDSVKGRFTISRDNKNNLYLQSSLSRSEDTGMYYGRSPYYDYVAFPTWGGGTIVTVS 120  
QY 118 S 118  
DB 121 A 121

Db 121 A 121

RESULT 9  
US-08-356-272-3  
; Sequence 3, Application US/08356272  
; Patent No. 5766946  
; GENERAL INFORMATION:  
; APPLICANT: Clantfiglia Dr., Maurizio  
; TITLE OF INVENTION: Monoclonal Antibodies to glycoprotein P  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patent and Trademark Department, Sandoz  
; STREET: 59 Route 10  
; CITY: East Hanover  
; STATE: N. J.  
; COUNTRY: U. S. A.  
; ZIP: 07936  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356, 272  
FILING DATE: 15-DEC-1994  
CLASSIFICATION: 435  
CLASSIFICATION: C12N5/20  
CLASSIFICATION: G01N33/574  
CLASSIFICATION: G01N33/577  
CLASSIFICATION: A61K39/295  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IT RM92A000457  
FILING DATE: 17-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP93/01533  
FILING DATE: 16-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Battle, Carl W.  
REGISTRATION NUMBER: 30, 731  
REFERENCE/DOCKET NUMBER: 118-8040  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 503-8177  
TELEFAX: (201) 503-8807  
TELEX: 240867  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-272-3

Query Match 79.3%; Score 502; DB 1; Length 123;  
Best Local Similarity 82.8%; Pred. No. 3.2e+43;  
Matches 101; Conservative 5; Mismatches 12; Indels 4; Gaps 2;

QY 1 OVQLOESGGGLVYK-PGSLKLSLSCAASGFTFSDYVYMWVROTPEKRLLEWVATISDGSSTYY 59  
DB 1 OVQLOESGGDLVKDPGSLKLSLSCAASGFTFSRYGMSWRQTDRKLEWVATISSGGSYY 60  
QY 60 YPDSVKGRTTISRDNANKNLTYLQMSLSKSEDTAMYCSF--YRTDDANDYGGCTTYTV 116  
DB 61 PPDVSKGRFTTISRDNANKNLTYLQVSSLSKSEDTAMYCARPAEFRGYSWFAVWGCGTYYTV 120  
QY 117 SS 118  
DB 121 SS 122

RESULT 10  
US-08-331-398A-65

; Sequence 65, Application US/08331398A  
; Patent No. 5608039  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Willingham, Mark  
; APPLICANT: Fitzgerald, David  
; APPLICANT: Brinkmann, Ulrich  
; APPLICANT: Pai, Lee  
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,398A  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-126110US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..125  
OTHER INFORMATION: /note="Mouse monoclonal antibody B5 Fv  
US-08-331-398A-65

Query Match 78.9%; Score 499.5; DB 1; Length 125;  
Best Local Similarity 80.7%; Pred. No. 5.7e+43;  
Matches 96; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

QY 1 OVQLOESGGGLVYKPGSLKLSLSCAASGFTFSDYVYMWVROTPEKRLLEWVATISDGSSTYY 60  
DB 1 EVKLVESGGGLVQPGSLKLSLSCATSGFTFSDYVYMWVROTPEKRLLEWVATISSGGSYY 60  
QY 61 PDSVKGRTTISRDNANKNLTYLQMSLSKSEDTAMYCSRYRYDDA-MDYVGGCTTYTVSS 118  
DB 61 PPTVKGRTTISRDNANKNLTYLQMSRLKSDTAMYCARGLSDGSWFAVWGCGTLYTVSS 119

RESULT 11  
US-08-331-397B-65  
; Sequence 65, Application US/08331397B  
; Patent No. 5981726  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira

APPLICANT: Benhar, Itai  
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-  
SPECIFIC ANTIBODY FRAGMENTS, FUSION PROTEINS, AND USES  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,397B  
FILING DATE: 28-OCT-1994  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 015280-12612005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ. ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..125  
OTHER INFORMATION: /note="Mouse monoclonal antibody B5 FV  
OTHER INFORMATION: Heavy chain region"  
US-08-331-397B-65  
Query Match 78.9%; Score 499.5; DB 2; Length 125;  
Best Local Similarity 80.7%; Pred. No. 5.7e-43;  
Matches 96; Conservative 7; Mismatches 15; Indels 1; Gaps 1;  
QY 1 QVQLSSGGGLVPRGSGIKSCASGFTPSDYMYWVWROTPERKLEWVAITSDGGSYTY 60  
DB 1 EVLVESGGGLVPGGSLKSCATSGFTPSDYMYWVWROTPERKLEWVAITSDGGSYTY 60  
QY 61 PDIVKGRFTISRDNAKNTLYLQMSLSKSEDTAMYYCRRYRDA-MDYWGCGTIVYSS 118  
DB 61 PDIVKGRFTISRDNAKNTLYLQMSLSKSEDTAMYYCARGLSDGSWPAWYWGCGTIVYSS 119  
RESULT 12  
US-08-759-804A-64  
Sequence 64, Application US/08759804A  
Patent No. 5990296  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Wittingham, Mark  
APPLICANT: Fitzgerald, David J.  
APPLICANT: Brinkmann, Ulrich  
APPLICANT: Pal, Lee  
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,  
STREET: Fusion Proteins, and Uses Thereof

NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/759,804A  
FILING DATE: 03-DEC-1996  
CLASSIFICATION: 536  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/331,398  
FILING DATE: 28-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/767,331  
FILING DATE: 30-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/596,289  
FILING DATE: 12-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 015280-12614005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ. ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..125  
OTHER INFORMATION: /note="Mouse monoclonal antibody B5 FV  
OTHER INFORMATION: Heavy chain region"  
US-08-759-804A-64  
Query Match 78.9%; Score 499.5; DB 2; Length 125;  
Best Local Similarity 80.7%; Pred. No. 5.7e-43;  
Matches 96; Conservative 7; Mismatches 15; Indels 1; Gaps 1;  
QY 1 QVQLSSGGGLVPRGSGIKSCASGFTPSDYMYWVWROTPERKLEWVAITSDGGSYTY 60  
DB 1 EVLVESGGGLVPGGSLKSCATSGFTPSDYMYWVWROTPERKLEWVAITSDGGSYTY 60  
QY 61 PDIVKGRFTISRDNAKNTLYLQMSLSKSEDTAMYYCRRYRDA-MDYWGCGTIVYSS 118  
DB 61 PDIVKGRFTISRDNAKNTLYLQMSLSKSEDTAMYYCARGLSDGSWPAWYWGCGTIVYSS 119  
RESULT 13  
US-08-579-378A-16  
Sequence 16, Application US/08579378A  
Patent No. 6210671  
GENERAL INFORMATION:  
APPLICANT: Co. Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco



STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/579,378A  
APPLICATION NUMBER: US/08/579,378A  
FILING DATE: 27-DEC-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160,074  
FILING DATE: 30-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,946  
FILING DATE: 01-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95112895.8  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95114696.8  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschultz, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 11823-002220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2422  
TELEFAX: 415-326-2400  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-579-378A-16

Query Match 78.8%; Score 499; DB 4; Length 135;  
Best Local Similarity 83.1%; Pred. No. 7e-43;  
Matches 98; Conservative 8; Mismatches 10; Indels 2; Gaps 2;

QY 1 OVOLDESGGLVPGGSLKSCAAGFTSDYYMYVWVROTPEKRLVMTISDGGSTYY 60  
DB 20 EVKLVEGGGLVPGGSLKSCAAGFTSTYAMSWVROTPEKRLVMTISDGGSTYY 78  
QY 61 PDVAGRFTISDNKNNLYLQMSLSKSEDTAMYYCSRYRDAMDYMGCGTTVYSS 118  
DB 79 PDVAGRFTISDNKNNLYLQMSLSKSEDTAMYYCAR-DYDGYFDYMGCGTTVYSS 135

RESULT 14  
US-08-661-052-4  
Sequence 4, Application US/08661052  
Patent No. 5837243  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deco  
APPLICANT: Joel Goldstein  
APPLICANT: Robert Graziano  
APPLICANT: Chezlan Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,052  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-661-052-4

Query Match 78.5%; Score 497; DB 2; Length 300;  
Best Local Similarity 76.7%; Pred. No. 2.8e-42;  
Matches 92; Conservative 13; Mismatches 13; Indels 2; Gaps 1;

QY 1 OVOLDESGGLVPGGSLKSCAAGFTSDYYMYVWVROTPEKRLVMTISDGGSTYY 60  
DB 1 EVOLVESGGGVQPGSLKSCSSSGFTSDNYMYVWVROPKGLVMTISDGGSTYY 60  
QY 61 PDVAGRFTISDNKNNLYLQMSLSKSEDTAMYYCSR--YRYDDAMDYMGCGTTVYSS 118  
DB 61 PDVAGRFTISDNKNNLYLQMSLSKSEDTAMYYCAR-DYDGYFDYMGCGTTVYSS 120

RESULT 15  
US-09-188-082-4  
Sequence 4, Application US/09188082  
Patent No. 6270765  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deco  
APPLICANT: Joel Goldstein  
APPLICANT: Robert Graziano  
APPLICANT: Chezlan Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/188,082  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/661,052  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400  
 TELEFAX: (617)227-5941  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 300 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 US-09-188-082-4

Query Match 78.5%; Score 497; DB 4; Length 300;  
 Best Local Similarity 76.7%; Pred. No. 2.8e-42;  
 Matches 92; Conservative 13; Mismatches 13; Indels 2; Gaps 1;

QY 1 OVOIQESGGGLVPRGSLKLSKASGFTFSDYVWYVROTPEKRLKLEWVATISDGGSYTY 60  
 Db 1 EVOLVESGGGVOPGRSLRLSCSSSGFTFSDNMYWVQAPEGLEWVATISDGGSYTY 60  
 QY 61 PDSYKGRFTISRDNKNNLYLQMSLSEPTAMYYCSR--YRYDDADYMGOGTTVYSS 118  
 Db 61 PDSYKGRFTISRDNKNNLYLQMSLSEPTAMYYCSR--YRYDDADYMGOGTTVYSS 120

Search completed: January 13, 2003, 15:13:42  
 Job time: 12.8 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:07:08 ; Search time 31.8087 Seconds  
(without alignments)  
494.317 Million cell updates/sec

Title: US-09-144-886-63

Perfect score: 633  
Sequence: 1 QVQLQESGGGLVFRGGSGLK.....YRVDAMDYMGCGITTVYSS 118

Scoring table

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A.Geneseq.101002:\*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*

2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*

3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*

4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*

5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*

6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:\*

7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:\*

8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:\*

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11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:\*

12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:\*

13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:\*

14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:\*

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16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:\*

17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:\*

18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:\*

19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*

20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*

21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*

22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*

23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575.5	90.9	123	21	AAV51266
2	568	89.7	120	15	AAV51266
3	550	86.9	115	21	AAV51266
4	532.5	84.1	142	14	AAV30882
5	532.5	84.1	249	22	AAV20434
6	532.5	84.0	159	18	AAV19575
7	522.3	82.5	217	16	AAV75460
8	520.5	82.2	119	23	AAV72814
9	520.5	82.2	464	23	AAV72801
10	519	82.0	120	17	AAV00240

11	513.5	81.1	119	16	AAV79876
12	513.5	81.1	119	18	AAV29994
13	513	81.0	118	16	AAV79161
14	510.5	80.6	119	16	AAV79887
15	510.5	80.6	138	21	AAV32404
16	510.5	80.6	239	21	AAV79866
17	509.5	80.5	117	16	AAV79155
18	509.5	80.5	117	16	AAV7357
19	509.5	80.5	117	18	AAV27354
20	507.5	80.2	119	16	AAV79888
21	507.5	80.2	121	21	AAV96063
22	507.5	80.2	140	23	AAV76122
23	506.5	80.0	143	21	AAV43867
24	505.5	79.9	121	23	AAE16426
25	504.5	79.7	120	13	AAV25204
26	504	79.6	118	15	AAV50323
27	504	79.6	118	16	AAV79153
28	503.5	79.5	119	23	AAV72813
29	502.5	79.4	138	13	AAV20064
30	502.5	79.4	139	14	AAV30480
31	502.5	79.4	140	23	AAV76132
32	502	79.3	123	15	AAV45187
33	501	79.1	118	19	AAV57576
34	501	79.1	118	20	AAV89627
35	501	79.1	118	21	AAV77502
36	501	79.1	118	22	AAV63382
37	501	79.1	118	22	AAV64764
38	501	79.1	118	22	AAV76880
39	501	79.1	118	22	AAV76899
40	501	79.1	118	22	AAV76918
41	501	79.1	118	23	AAV95197
42	501	79.1	137	19	AAV57592
43	501	79.1	137	20	AAV89625
44	501	79.1	137	21	AAV77513
45	501	79.1	137	22	AAV67102

#### ALIGNMENTS

RESULT 1	
AAV51266	
ID	AAV51266 standard; peptide; 123 AA.
AC	AAV51266;
XX	
DT	14-APR-2000 (first entry)
XX	
DE	Monoclonal antibody MAK 33 heavy chain variable region peptide.
XX	
KW	Framework region; monoclonal antibody; variable domain; detection;
KW	Immunotherapy; MAK 33.
XX	
OS	Unidentified.
XX	
PN	DE19828466-A1.
XX	
PD	30-DEC-1999.
XX	
PF	26-JUN-1998; 98DE-1028466.
XX	
PR	26-JUN-1998; 98DE-1028466.
XX	
PA	(HOFF) ROCHE DIAGNOSTICS GMBH.
XX	
PI	Nussbaum S, Moesner E, Lenz H, Praest G;
XX	
DR	WPI; 2000-107255/10.
XX	
PT	Suppressor peptides derived from antibodies for use in immunoassays
XX	
PS	Disclosure; Page 18; 20pp; German.
XX	

CC This invention describes novel peptides derived from a framework region  
CC of the variable domain of an antibody for detection, immunotherapy or  
CC for scintigraphy. The peptides of the invention are used in a method to  
CC detect analytes in a sample by eliminating interference in the sample.  
CC AAY51254-Y51267 represent peptides derived from the framework regions of  
CC the variable domain of an antibody which are used to illustrate the  
CC method of the invention.

CC Sequence 123 AA;

Query Match 90.9%; Score 575.5; DB 21; Length 123;  
Best Local Similarity 89.4%; Pred. No. 3e-46;  
Matches 110; Conservative 4; Mismatches 4; Indels 5; Gaps 1;

QY 1 QVLOESGGGLVPRGSLKSCAASGFTFSDYMWVWVROTPERKLEWVATISDGGSTYY 60  
Db 1 EVQVSEGGGLVPRGSLKSCAASGFTFSDYMWVWVROTPERKLEWVATISDGGSTYY 60  
QY 61 PDSVKGFTISRDNKAKNNLYLQMSLSKSEDTAMVYCSRYR---YDADMDYWGQGTYY 115  
Db 61 PDSVKGFTISRDNKAKNNLYLQMSLSKSEDTAMVYCARDKAYGNGDAMDYWGQGTYY 120  
QY 116 VSS 118  
Db 121 VSS 123

## RESULT 2

AAR54931

ID AAR54931 standard; peptide; 120 AA.

AC AAR54931;

DT 19-OCT-1994 (first entry)

DE Fc receptor Mab 022 VH chain.

KW Fc receptor; FcR; humanized antibody; hab; IgG; cancer; allergy;

KW autoimmune disease; heteroantibody; bifunctional antibody;

KW immunotoxin; CDR; complementarity determining region; VH;

KW heavy chain variable region; VK; kappa chain variable region;

KW mononuclear phagocyte; PCR; polymerase chain reaction; primer;

KW site-directed mutagenesis; monoclonal antibody; Mab.

OS Mus sp.

PN WO9410332-A.

PD 11-MAY-1994.

PF 04-NOV-1993; 93WO-US10384.

PR 04-NOV-1992; 92GB-0023377.

PA (MEDA-) MEDAREX INC.

PI Carr FT, Harris WJ, Tempest PR;

PI WPI; 1994-167486/20.

PT New humanised antibodies to Fc receptors - used for diagnosis or  
PT for treatment of e.g. cancer, allergies and infectious and  
PT auto-immune diseases

PS Disclosure; Page 15; 36pp; English.

CC Humanized antibodies (habs) for IgG Fc receptors on human phagocytes  
CC comprise the CDR of mouse monoclonal antibody 22 (from hybridoma  
CC 022MCL-1), VH chains from human Igs NEMM or KOL, and VK chains from  
CC Ig RFI. Sequences are provided for mouse 022 VH (AAR54931),  
CC humanized NEMM-based VH (022 NMVH, AAR54929), humanized KOL-  
CC based VH (022 KLVH, AAR54930), mouse 022 VK (AAR54933) and humanized  
CC RFI-based VK (022 HUVK, AAR54932). During hab production, VH and VK

CC cDNAs were PCR amplified using primers given in AA065378-87.  
CC Mutagenesis of clone M13VHPCR2 KOL VH (L71R) was performed using  
CC oligos AA065388-89. The habs can be used in heteroantibody,  
CC bifunctional antibody and immunotoxin production.

CC Sequence 120 AA;

Query Match 89.7%; Score 568; DB 15; Length 120;  
Best Local Similarity 89.2%; Pred. No. 1.5e-45;  
Matches 107; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

QY 1 QVLOESGGGLVPRGSLKSCAASGFTFSDYMWVWVROTPERKLEWVATISDGGSTYY 60  
Db 1 EVQVSEGGGLVPRGSLKSCAASGFTFSDYMWVWVROTPERKLEWVATISDGGSTYY 60  
QY 61 PDSVKGFTISRDNKAKNNLYLQMSLSKSEDTAMVYCSRYR---YDADMDYWGQGTYY 118  
Db 61 PDSVKGFTISRDNKAKNNLYLQMSLSKSEDTAMVYCARDKAYGNGDAMDYWGQGTYY 120

## RESULT 3

AAB12460

ID AAB12460 standard; protein; 115 AA.

AC AAB12460;

DT 25-OCT-2000 (first entry)

DE IgG monoclonal antibody protein sequence SEQ ID NO:6.

KW Monoclonal antibody; hybridoma cell; immunoglobulin; IgG; fusion;

KW human albumin; diabetic nephropathy; diagnosis.

OS Mus musculus.

PN JP2000139460-A.

PD 23-MAY-2000.

PF 02-NOV-1998; 98JP-0311677.

PR 02-NOV-1998; 98JP-0311677.

PA (TOYOTA) TOYOTA CHUO KENKYUSHO KK.

PA (AISE) AISEN SEIKI KK.

DR WPI; 2000-433935/38.

DR N-PADB; AAA60723.

PT Hybridoma cells for preparation of IgG monoclonal antibody capable of  
PT rapid reaction with human albumin for diagnosis of diabetic nephropathy

PS Disclosure; Page 8; 11pp; Japanese.

CC The present invention describes hybridoma cells used for preparing an  
CC immunoglobulin G (IgG) monoclonal antibody capable of rapid reaction  
CC with human albumin. The hybridoma cells are prepared by fusion of mam-  
CC myeloma cells and spleen cells immunised with human serum albumin, and  
CC producing IgG monoclonal antibody which rapidly react with human  
CC albumin. The monoclonal antibodies can be used in the diagnosis of  
CC diabetic nephropathy. The present sequence represents an IgG monoclonal  
CC antibody protein sequence from the present invention.

CC Sequence 115 AA;

Query Match 86.9%; Score 550; DB 21; Length 115;  
Best Local Similarity 89.7%; Pred. No. 6.7e-44;  
Matches 105; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 2 VQLOESGGGLVPRGSLKSCAASGFTFSDYMWVWVROTPERKLEWVATISDGGSTYY 61  
Db 1 VQLOESGGGLVPRGSLKSCAASGFTFSDYMWVWVROTPERKLEWVATISDGGSTYY 60

OY 62 DSVKGRFTISRDNANKNNLYLQMSLSKSEDTAMYYCSRYRDAMDYWGCGTTVTYSS 118  
 DB 61 DSVKGRFTISRDNANKNNLYLQMTSLKSEDTAMYYCVRGEMNGA--YWGCGTTVTYSS 115

## RESULT 4

ID AAR30882 standard: Protein: 142 AA.

XX AAR30882;

XX 10-MAY-1993 (first entry)

XX Antibody 4A2 heavy chain constant region.

XX Fd'; fragment; human; 4A2; constant region; Fab'; F(ab')2; antibody;  
 heavy chain; primer.

XX Mus musculus.

XX WO9222324-A.

XX 23-DEC-1992.

XX 15-JUN-1992; 92WO-US04976.

XX 14-JUN-1991; 91US-0714175.

XX (XOMA ) XOMA CORP.

XX Better MD, Carroll S, Horwitz AH;

XX WPI: 1993-017909/02.

XX P-PSDB: AAQ34576.

XX Polynucleotide sequences encoding Fab' and F(ab')2 fragments -  
 used to produce, e.g. antibody-ricin A chain immuno:toxin(s)

XX Disclosure: Fig 11; 92pp; English.

XX This sequence represents the heavy chain constant domain (CH) from  
 CC mouse antibody 4A2. This sequence was used in conjunction  
 CC with the Fd' sequences given in AAQ34567-72 to produce chimeric Fd'  
 CC vectors.

XX Sequence 142 AA;

Query Match 84.1%; Score 532.5; DB 14; Length 142;  
 Best Local Similarity 83.7%; Pred. No. 3,6e-42;  
 Matches 103; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

OY 1 OVQLOESGGGLVPGGSLKLSCAASGFTFSDYMYVVRQTPKRLKLEWVATISDGSSTYY 60  
 DB 20 EVQLVESGGGLVPGGSLKLSCAASGFTFSDYMYVVRQTPKRLKLEWVATISDGSSTYY 79

OY 61 PDSVGRFTISRDNANKNNLYLQMSLSKSEDTAMYYCSR--YRDA--MDYWGCGTTVT 115  
 DB 80 SDSYGRFTISRDNANKNNLYLQISSLSKSEDTAMYYCARDPYSYDSSPAMFAWGGTTLVT 139

OY 116 VSS 118

DB 140 VSA 142

RESULT 5  
 AAB20434  
 ID AAB20434 standard: Protein: 249 AA.

XX AAB20434;

XX 21-JUN-2001 (first entry)

DE Anti-FIX/FIXa antibody 193/K2 scFv.

XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;

XX Factor VIII cofactor; blood coagulation disorder; haemophilia A;

XX haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

XX Chimeric - Mus musculus.

XX Chimeric - Synthetic.

XX Key

XX Location/Qualifiers

XX 1..121

XX /label= VH

XX Region

XX /label= CDR3

XX Peptide

XX /label= Linker

XX Protein

XX /label= VL

XX Region

XX /label= CDR3

XX WO200119992-A2.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-EP08936.

XX 14-SEP-1999; 99AT-0001576.

XX (BAXT ) BAXTER AG.

XX Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;

XX WPI: 2001-290358/30.

XX N-PSDB: AAF30724.

XX New factor IX/factor IXa antibodies and their derivatives useful for

XX increasing amidolytic activity of factor IXa, and for treating blood

XX coagulation disorders such as haemophilia A and haemorrhagic diathesis

XX Claim 10; Fig 15; 138pp; English.

XX The present sequence is that of a single chain Fv (scFv) derivative

XX of antibody 193/K2, comprising the heavy (VH) and light (VL) chain

XX variable regions of 193/K2 joined by an artificial, flexible linker

XX peptide. The scFv was obtained by PCR amplification of cDNAs for

XX CC 193/K2 VH and VL regions and cloning in vector pDAp2. 193/K2 is

XX an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)

XX antibodies of the invention. Anti-FIX/FIXa and their derivatives,

XX including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor

XX activity or FIXa activating activity. Administration leads to an

XX increase in the procoagulant activity of FIXa, even in the presence

XX of FVIIIa inhibitors. This allows for rapid blood coagulation even

XX in the absence of FVIII or FVIIIa, and in the case of FVIII

XX inhibitor patients. The antibodies and derivatives are used in a

XX claimed pharmaceutical composition for treating patients with blood

XX coagulation disorders, especially haemophilia A and haemorrhagic

XX diathesis.

XX Sequence 249 AA;

Query Match 84.1%; Score 532.5; DB 22; Length 249;  
 Best Local Similarity 84.3%; Pred. No. 6,5e-42;  
 Matches 102; Conservative 6; Mismatches 10; Indels 3; Gaps 1;

OY 1 OVQLOESGGGLVPGGSLKLSCAASGFTFSDYMYVVRQTPKRLKLEWVATISDGSSTYY 60  
 DB 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSDYMYVVRQTPKRLKLEWVATISDGSSTYY 60

OY 61 PDSVGRFTISRDNANKNNLYLQMSLSKSEDTAMYYCSR--YRDAAMDYWGCGTTVTYSS 117  
 DB 61 PDSVGRFTISRDNANKNNLYLQMSLSKSEDTAMYYCTRDGCHGYGSSFDYWGCGTTVTYSS 120

Oy		118 S 118	
Db	121 S 121		
RESULT 6			
ID	AAM19575		
XX	AAM19575 standard; Protein; 159 AA.		
XX			
XX			
XX			
XX	30-JUL-1997 (first entry)		
DE	Mouse anti-idiotypic antibody. 15H8 heavy chain variable region.		
XX			
KW	Anti-idiotypic; anti-EGFR; epidermal growth factor receptor; tumour;		
RW	cancer; neoplasia; glioma; melanoma; carcinoma; drug; manufacture; ss		
OS	Mus musculus.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT		/label= sig.peptide	
FT		20..49	
FT	Region	/label= FR1	
FT		/note= "framework region 1"	
FT	Region	50..54	
FT		/label= CDRI	
FT	Region	/note= "complementarity determining region 1"	
FT		55..68	
FT		/label= FR2	
FT	Region	/note= "framework region 2"	
FT		69..85	
FT	Region	/label= CDR2	
FT		/note= "complementarity determining region 2"	
FT	Region	86..117	
FT		/label= FR3	
FT	Region	/note= "framework region 3"	
FT		118..134	
FT	Region	/label= CDR3	
FT		/note= "complementarity determining region 3"	
FT	Region	135..145	
FT		/label= FR4	
FT	Region	/note= "framework region 4"	
FT		146..159	
FT	Region	/note= "mouse constant Iggi region"	
XX			
PN	EP745612 A1.		
XX			
PD	04-DEC-1996.		
XX			
PE	14-MAY-1996;	96EP-0107651.	
XX			
PR	26-MAY-1995;	95EP-0107967.	
XX	(MERE ) MERCK PATENT GMBH.		
XX			
PI	Adan J, Carceller A, Gomez A, Plutats J, Rosell E;		
DR	WPL: 1997-013659/02.		
DR	N-PSTDB: MAT70806.		
PT	Monoclonal anti-idiotypic antibodies mimicking epidermal growth		
PS	factor receptor - useful for tumour therapy		
PS	Claim 6; Fig 5A; 28pp; English.		
CC	Murine monoclonal anti-idiotypic antibodies, 15H8, 3B6 and 5A6 are		
CC	new. They induce an immune response against epidermal growth factor		
CC	receptor (EGFR). The sequences of the heavy and light chain variable		
CC	regions of these antibodies are given in the specification. The		
CC	antibodies are used for the manufacture of drugs directed against		
CC	tumours that express EGFR on their surface, including melanomas,		

[illegible]

CC diagnosis, e.g. detection of the immunorecessive antigen, or in therapy  
CC e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia.  
CC The method of production of the antibody allows rapid and sensitive  
CC isolation of antibodies that would be difficult to isolate by standard  
CC methods. The antibodies produced have greater binding affinity than  
CC those produced by combinatorial/hybridoma methods.  
XX  
SO Sequence 217 AA;  
Query Match 82.5%; Score 522.5; DB 16; Length 217;  
Best Local Similarly 84.7%; Pred. No. 4.8e-41;  
Matches 100; Conservative 6; Mismatches 9; Indels 3; Gaps 1;  
OY 1 QVLOESGCGLVKPGSGSLKSCAASGFTFSDYMWVWQTEPKRLRWATISDGSYTY 60  
DB 1 EVKLMESSGDLVKKPGSGSLKSCAASGFTFSDYMWVWQTEPKRLRWATISDGSYTY 60  
OY 61 PDSYKGRFTISRDNANKNNLYLQMSLKSSEDYAMYCSRRYRDDAMDYGGGTTVYSS 118  
DB 61 ADSYKGRFTISRDNANKNNLYLQMSLKSSEDYAMYCAR---DPLXGSGGGTTLVYSS 115  
RESULT 8  
AAU72814  
ID AAU72814 standard; Protein: 119 AA.  
XX  
AC AAU72814;  
XX  
DT 26-FEB-2002 (first entry)  
XX  
DE Humanised mouse TRA-8 anti-human DR5 antibody #4.  
XX  
KW Tumour necrosis factor-related apoptosis-inducing ligand receptor;  
KW TRAIL; TRAIL receptor DR5; cytosolic; apoptosis; cell proliferation;  
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;  
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;  
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;  
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.  
XX  
OS Synthetic.  
XX  
PN WO200183560-A1.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14151.  
XX  
PR 02-MAY-2000; 2000US-201344P.  
XX  
PA (UABR-) UAB RES FOUND.  
XX  
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;  
XX WPI: 2002-049338/06.  
XX  
DR WPI: 2002-049338/06.  
XX  
PT Novel antibody specific for tumour necrosis factor-related  
PT apoptosis-inducing ligand, useful for inhibiting cell proliferation in  
PT cancer -  
XX  
XX Example 26; Page 212-213; 229pp; English.  
XX  
XX The invention describes a novel antibody which recognizes a tumour  
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor  
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing  
CC activity to a cell expressing DR5 in vivo. It is also useful for  
CC preparing a therapeutic for selective apoptosis of abnormal or  
CC dysregulated cells, and for inhibiting cell proliferation in a cell,  
CC preferably a human breast, ovary, colon, haematopoietic, prostate,  
CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may  
CC also be administered e.g. paclitaxel, taxol or cycloheximide. The  
CC antibody is used to treat an autoimmune disease, systemic lupus

CC erythematosus, Hashimoto's disease, rheumatoid arthritis.  
CC graft-versus host disease, Sjogren's syndrome, Chron's disease,  
CC pernicious anaemia, Addison disease, scleroderma, Goodpasture's syndrome,  
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple  
CC sclerosis, Basedow's disease, insulin-dependent diabetes mellitus,  
CC allergy, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,  
CC glomerular nephritis, hypoplastic anaemia, rejection after organ  
CC transplantation, and numerous malignancies of lung, prostate, liver,  
CC ovary, lymphatic or breast tissue. This sequence shows one of the  
CC humanised anti-DR5 antibodies described in the method of the invention.  
XX  
SO Sequence 119 AA;  
Query Match 82.2%; Score 520.5; DB 23; Length 119;  
Best Local Similarly 85.0%; Pred. No. 3.9e-41;  
Matches 102; Conservative 5; Mismatches 10; Indels 3; Gaps 2;  
OY 1 QVLOESGCGLVKPGSGSLKSCAASGFTFSDYMWVWQTEPKRLRWATISDGSYTY 60  
DB 1 EVKLMESSGCGLVKPGSGSLKSCAASGFTFSSYVMSVWQTEPKRLRWATISDGSYTY 60  
OY 61 PDSYKGRFTISRDNANKNNLYLQMSLKSSEDYAMYCSRRYRDDAM--DYWGCGTTVYSS 118  
DB 61 PDSYKGRFTISRDNANKNNLYLQMSLKSSEDYAMYCAR--RGDSMTTDDYWGCGTTLVYSS 119  
RESULT 9  
AAU72801  
ID AAU72801 standard; Protein: 464 AA.  
XX  
AC AAU72801;  
XX  
DT 26-FEB-2002 (first entry)  
XX  
DE TRA-8 heavy chain.  
XX  
KW Tumour necrosis factor-related apoptosis-inducing ligand receptor;  
KW TRAIL; TRAIL receptor DR5; cytosolic; apoptosis; cell proliferation;  
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;  
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;  
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;  
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.  
XX  
XX Mus musculus.  
XX  
OS  
XX  
PN WO200183560-A1.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14151.  
XX  
PR 02-MAY-2000; 2000US-201344P.  
XX  
PA (UABR-) UAB RES FOUND.  
XX  
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;  
XX WPI: 2002-049338/06.  
XX  
DR N-PSDB; AAS97062.  
XX  
PT Novel antibody specific for tumour necrosis factor-related  
PT apoptosis-inducing ligand, useful for inhibiting cell proliferation in  
PT cancer -  
XX  
XX Claim 26; Page 198-199; 229pp; English.  
XX  
XX The invention describes a novel antibody which recognizes a tumour  
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor  
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing  
CC activity to a cell expressing DR5 in vivo. It is also useful for  
CC preparing a therapeutic for selective apoptosis of abnormal or





PR 17-MAR-1994; 94EP-0104160.  
 XX (MERE ) MERCK PATENT GMBH.  
 XX  
 PI Adan J, Ansell KH, Bendig MM, Blasco F, Guessow D;  
 PI Kettleborough AC, Mijans F, Piuels J, Rosell E;  
 XX  
 DR WPI: 1995-336972/43.  
 XX  
 PT Anti-EGFR antibodies and single chain Fv antibody fragments -  
 PT obtained from phage-antibody libraries, useful for diagnosis and  
 PT therapy of tumours  
 XX  
 PS Disclosure: Figure 1A; 93pp; English.  
 XX  
 CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies  
 CC and antibodies constructed from anti-EGFR antibody fragments can be  
 CC used for diagnosis of tumours and assessment of tumour growth in  
 CC vitro and in vivo. They may also be used in a pharmaceutical  
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.  
 CC The antibodies and fragments are derived from mice but are humanised  
 CC so as to cause minimum reaction against them. They are produced  
 CC using the phage antibody library. (See AAT04011-T04026 and  
 CC AAR79858-R79873)  
 CC  
 XX  
 SQ Sequence 119 AA:  
 Query Match 81.1%; Score 513.5; DB 16; Length 119;  
 Best Local Similarity 84.9%; Pred. No. 1.7e-40;  
 Matches 101; Conservative 5; Mismatches 12; Indels 1; Gaps 1;  
 OY 1 OVQLOESGGGLVKGPGSLKLSCAASGFTPSDYVMVWVROTPEKRLFWATISDGSYTY 60  
 Db 1 OVQLOESGGDLVKGPGSLKLSCAASGFTPSDYVMVWVROTPEKRLFWATISDGSYTY 60  
 OY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRYRYD-AMDYWGQGTTVVSS 118  
 Db 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCARLETDGYALDYWGQGTTVVSS 119

RESULT 12  
 AAM29994  
 ID AAM29994; standard; protein; 119 AA.  
 XX  
 AC AAM29994;  
 XX  
 DT 12-MAR-1998 (first entry)  
 XX  
 DE Heavy chain variable region of MAb for t1A.  
 XX  
 DE Heavy chain variable region of MAb for t1A.  
 XX  
 KW Heavy chain: variable region; monoclonal antibody; human; CD6; murine;  
 KW leukocyte differentiation antigen; hybridoma; humanisation; mutagenesis;  
 KW PCR; primer: amplification; inflammatory infiltration; skin; psoriasis;  
 KW diagnosis.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9719111-A2.  
 XX  
 PD 29-MAY-1997.  
 XX  
 PF 18-NOV-1996; 96MO-CU00004.  
 XX  
 PR 17-NOV-1995; 95CU-0000120.  
 XX  
 PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.  
 XX  
 PI Lombardero Valladares J, Montero Casimiro JE, Perez Rodriguez R;  
 PI Sierra Blazquez P, Tormo Bravo BR;  
 XX  
 DR WPI: 1997-298060/27.  
 XX  
 PT Monoclonal antibody against human CD6 antigen - useful for diagnosis

PT and treatment of psoriasis  
 XX  
 PS Claim 3; Page 27; 36pp; Spanish.  
 XX  
 CC This is the amino acid sequence of the heavy chain variable region  
 CC of the monoclonal antibody (MAb) for t1A which recognises the human  
 CC leukocyte differentiation antigen CD6. The MAb is a murine IgG2-type  
 CC Ab produced by the usual hybridoma techniques. The coding sequence  
 CC for the variable region can be used to generate humanised variants,  
 CC especially by mutagenic PCR. CD6 has been shown to be expressed in  
 CC T lymphocytes involved in the inflammatory infiltration of the skin  
 CC in psoriasis. The anti-CD6 MAb can therefore be used to diagnose and  
 CC treat psoriasis.  
 XX  
 SQ Sequence 119 AA:  
 Query Match 81.1%; Score 513.5; DB 18; Length 119;  
 Best Local Similarity 84.0%; Pred. No. 1.7e-40;  
 Matches 100; Conservative 4; Mismatches 14; Indels 1; Gaps 1;  
 OY 1 OVQLOESGGGLVKGPGSLKLSCAASGFTPSDYVMVWVROTPEKRLFWATISDGSYTY 60  
 Db 1 EVQLVESGGGLVKGPGSLKLSCAASGFKFSRYAMSVWVROTPEKRLFWATISGGSYTY 60  
 OY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRYRYD-DAMDYWGQGTTVVSS 118  
 Db 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCARLDYDLDYFDSWGQGTTLTVSS 119

RESULT 13  
 AAR79161  
 ID AAR79161; standard; peptide; 118 AA.  
 XX  
 AC AAR79161;  
 XX  
 DT 04-MAR-1996 (first entry)  
 XX  
 DE Human IgE receptor-binding antibody-related peptide heavy chain.  
 XX  
 KW Immunoglobulin E; antibody; receptor; monoclonal; detection;  
 KW complementarity determining region.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FH Region 29..33  
 FT /label= CDR1H  
 FT /note= "all CDR regions are claimed"  
 FT Region 48..64  
 FT /label= CDR2H  
 FT /note= "all CDR regions are claimed"  
 FT Region 97..107  
 FT /label= CDR3H  
 FT /note= "all CDR regions are claimed"  
 XX  
 PN JP07165799-A.  
 XX  
 PD 27-JUN-1995.  
 XX  
 PF 22-OCT-1993; 93UP-0264792.  
 XX  
 PR 22-OCT-1993; 93UP-0264792.  
 XX  
 PA (ASAK ) ASAKI BREWERIES LTD.  
 PA (NIKK-) NIKKA WHISKY KK.  
 PA (TORI ) TORII YAHUKIN KK.  
 PA (TSUR/) TSURA T.  
 XX  
 DR WPI: 1995-261292/34.  
 XX  
 DR N-PSDB: AAO96288.  
 XX  
 PT Novel monoclonal antibody against human high-affinity IgE receptor -  
 PT and DNA fragment encoding the MAb, for the specific identification

PT of human Fc-epsilon RI  
XX  
XX Claim 9; Page 16; 20pp; Japanese.  
XX  
CC Polypeptides which specifically recognise human IgE receptor (Fc-  
CC epsilon-RI) have been isolated and sequenced. The new peptides are  
CC related to a monoclonal antibody against Fc-epsilon-RI and are  
CC either heavy or light chain molecules. The heavy chain molecules  
CC have the general formula FRI-CDRIH-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.  
CC to AAR79153, AAR79155, AAR79157, AAR79159 and AAR79161) and are encoded  
CC by AAO96280, AAO96282, AAO96284, AAO96286 and AAO96288. FRI is a  
CC polypeptide having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide,  
CC FR3 is a 33-35aa polypeptide and FR4 is a 12-14 aa polypeptide.  
CC Similarly the light chains have the general formula  
CC FR5-CDRIH-FR6-CDR2L-FR7-CDR3L-FR8, (corresp. to AAR79154, AAR79156,  
CC AAR79158, AAR79160 and AAR79162) and are encoded by AAO96281, AAO96283,  
CC AAO96285, AAO96287 and AAO96289. FR5 is a 23-28 aa polypeptide, FR6 is a  
CC 14-16 aa polypeptide, FR7 is a 30-34 aa polypeptide and FR8 is a 9-11 aa  
CC polypeptide. All the peptides are derived from mouse hybridoma cells and  
CC are useful in the detection of the human Fc-epsilon-RI or for the  
CC elucidation of an antigen recognising region of a monoclonal antibody  
CC against human Fc-epsilon-RI.  
XX  
SQ Sequence 118 AA;  
Query Match 81.0%; Score 513; DB 16; Length 118;  
Best Local Similarity 82.5%; Pred. No. 1.9e-40;  
Matches 99; Conservative 8; Mismatches 9; Indels 4; Gaps 2;  
OY 1 QVQLQESGGGLVPRGSGSLKSCAASGFTFSDYIMYWRQTPERKLEWVAITISDGGSTYY 60  
DB 1 QVRLQDSGGGLVPGGSLKSCATSCGFT--DYMFVWRQTPERKLEWVAITISDGGSTYY 58  
OY 61 PDSVKGRTTISRDNAKNTLTQMSLSKSEPTAMVYCSRR--YRYDADMDYWGQTTVYSS 118  
DB 59 PDYVKGRTTISRDNAKNTLTQMSLSKSEPTAMVYCARNGTRIGYAVDYGQTTVYSS 118  
RESULT 14  
AAR79887  
ID AAR79887 standard; Protein; 119 AA.  
XX  
AC AAR79887;  
XX  
XX 02-JUL-1996 (first entry)  
DE Anti-EGFR antibody heavy chain variable region (Clone S4 10H).  
XX  
XX Single chain antibody; antibody; epidermal growth factor receptor;  
KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;  
KW assessment; phage antibody library.  
XX  
OS Mus musculus.  
XX  
XX  
FH Key Location/Qualifiers  
FT Region 1..30  
FT /label= Framework region 1.  
FT Region 31..35  
FT /label= CDR1.  
FT Region 36..49  
FT /label= Framework region 2.  
FT Region 50..66  
FT /label= CDR2.  
FT Region 67..98  
FT /label= Framework region 3.  
FT Region 99..108  
FT /label= CDR3.  
FT Region 109..119  
FT /label= Framework region 4.  
PN WO9525167-A1.  
XX  
XX 21-SEP-1995.

XX  
XX 16-MAR-1995; 95WO-EP00978.  
XX  
XX 02-DEC-1994; 94EP-0118970.  
PR 17-MAR-1994; 94EP-0104160.  
XX  
XX (MERE) MERCK PATENT GMBH.  
PI Aadan J, Ansell KH, Bendig MM, Biasco F, Guessow D;  
PI Kettleborough AC, Miltjans F, Piuilats J, Rosell E;  
XX WPI; 1995-336972/43.  
DR  
XX  
XX Anti-EGFR antibodies and single chain Fv antibody fragments  
PT obtained from phage-antibody libraries, useful for diagnosis and  
PT therapy of tumours  
XX  
XX Disclosure; Figure 1B; 93pp; English.  
XX  
XX Anti-epidermal growth factor receptor (EGFR) single chain antibodies  
CC and antibodies constructed from anti-EGFR antibody fragments can be  
CC used for diagnosis of tumours and assessment of tumour growth in  
CC vitro and in vivo. They may also be used in a pharmaceutical  
CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.  
CC The antibodies and fragments are derived from mice but are humanised  
CC so as to cause minimum reaction against them. They are produced  
CC using the phage antibody library. (See AAT04011-T04026 and  
CC AAR79858-R79873)  
XX  
SQ Sequence 119 AA;  
Query Match 80.6%; Score 510.5; DB 16; Length 119;  
Best Local Similarity 84.0%; Pred. No. 3.3e-40;  
Matches 100; Conservative 6; Mismatches 12; Indels 1; Gaps 1;  
OY 1 QVQLQESGGGLVPRGSGSLKSCAASGFTFSDYIMYWRQTPERKLEWVAITISDGGSTYY 60  
DB 1 EVKLQESGGGLVPRGSGSLKSCAASGFTFSYGSWVRQTPDRLSVAITISGGAYIYY 60  
OY 61 PDSVKGRTTISRDNAKNTLTQMSLSKSEPTAMVYCSRRYRD--AMDYWGQTTVYSS 118  
DB 61 PDYVKGRTTISRDNAKNTLTQMSLSKSEPTAMVYCARLETGTALDYWGQTTVYSS 119  
RESULT 15  
AAV32404  
ID AAV32404 standard; Protein; 138 AA.  
XX  
AC AAV32404;  
XX  
XX 13-MAR-2000 (first entry)  
DE Mouse anti-verotoxin II antibody VTM1-1 heavy chain variable region.  
XX  
XX Verotoxin II; VT2; shiga-like toxin; VTM1-1; MuVTM1-1;  
KW monoclonal antibody; heavy chain; mouse; humanised antibody;  
KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome;  
KW HUS; therapy.  
XX  
OS Mus musculus.  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /note= "signal peptide"  
FT Protein 20..138  
FT /note= "mature protein"  
FT Region 50..54  
FT /note= "complementarity determining region 1"  
FT Region 55..85  
FT /note= "complementarity determining region 2"  
FT Region 86..127  
FT /note= "complementarity determining region 3"  
XX

```

PN      WO9959629-A1.
XX
PD      25-NOV-1999.
XX
PF      19-MAY-1999; 99WO-US11179.
XX
PR      20-MAY-1998; 98US-0086570.
XX
PA      (TEIJ ) TEIJIN LTD.
XX      (PROT-) PROTEIN DESIGN LABS INC.
PI      Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;
XX      WPI: 2000-086580/07.
DR      N-PSDB: AA235241.
XX
PF      Humanized antibody binding to verotoxin II used for treating Verotoxin
PT      producing E. coli.
XX
PS      Claim 5; Fig 1a; 59pp; English.
XX
CC      This sequence represents the heavy chain variable region of murine
CC      monoclonal antibody Vtm1-1 (MuVTm1-1), an antibody that specifically
CC      binds to the B subunit of verotoxin II (VT2). The invention relates
CC      to humanised antibodies against VT2 that are capable of neutralizing
CC      VT2 and/or VT2 variants. The humanised antibody is a humanized form
CC      of MuVTm1-1 comprising the complementarity determining regions of
CC      MuVTm1-1 and the heavy and light chain variable region frameworks
CC      from the human G4 antibody heavy and light chain frameworks,
CC      provided that at least 1 position selected from I49, H29, H30, H49
CC      and H98 is occupied by the amino acid at the equivalent position of
CC      the MuVTm1-1 antibody heavy or light chain variable region framework.
CC      Such humanized antibodies (see AAY32406-07) have an affinity for VT2
CC      that is 3-, 5 or 10-times that of MuVTm1-1. They are used for
CC      treating a patient suffering from, or at risk of, the toxic effects
CC      from VT2 (claimed), especially for treating verotoxin producing
CC      Escherichia coli (VTEC) infection, and haemolytic uraemic syndrome
CC      (HUS).
XX
SQ      Sequence 138 AA:
      Query Match 80.6%; Score 510.5; DB 21; Length 138;
      Best Local Similarity 83.5%; Pred. No. 3.9e-40;
      Matches 101; Conservative 6; Mismatches 9; Indels 5; Gaps 2;

OY      1 QVQLDSESGELVKGPGSLKSCAASGFTFSDIYMTWVROTPPKRLRWATISDGGSYTY 60
      :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      20 EVQLVESGGGLVKGPGSLKSCAASGFTFSYGMWVROTPPKRLRWATISTGGSYTY 79
OY      61 PDSTVGRFTISRDNAKNNLYLQMSSILKSEDTAMYYCSRIRYDQ---MDYWGCGTTVTYS 117
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      80 PDSTVGRFTISRDNAKNNLYLQMSSILKSEDTAITYCA--RQGDAMGNLDYWGCGTSYTVS 137
OY      118 S 118
      |
DB      138 S 138

```

Search completed: January 13, 2003, 15:11:17  
 Job time : 33.8087 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:09:39 : Search time 24.3478 Seconds  
(without alignments)  
947.817 Million cell updates/sec

Title: US-09-144-886-87

Perfect score: 586

Sequence: 1 DIETQSPASLAVSLGQRAT.....QGSNEDPFTFGSGTKLEIKR 112

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	80.4	111	11	Q920E9 mus musculus
2	439	74.9	103	11	Q91180 mus musculus
3	386	65.9	108	4	Q9UL77 homo sapien
4	383	65.4	108	4	Q9UL70 homo sapien
5	380.5	64.9	107	4	Q96SA9
6	377.5	64.4	238	11	Q99M37
7	375.5	64.1	109	4	Q9UL78
8	370	63.1	214	11	Q9RIAS
9	369.5	63.1	107	4	Q9UL81
10	367	62.6	108	4	Q9UL83
11	366.5	62.5	238	11	Q9VC16
12	365	62.3	234	11	Q91WF8
13	362	61.8	108	4	Q9UL79
14	357.5	61.0	239	11	Q8TCDO
15	357.5	61.0	239	11	Q8VC55
16	356	60.8	234	11	Q8R062

17	351.5	60.0	109	4	Q9UL85	Q9UL85 homo sapien
18	351	59.9	234	11	Q8VCP0	Q8VCP0 mus musculus
19	350	59.7	114	4	Q9UL80	Q9UL80 homo sapien
20	349.5	59.6	109	4	Q9UL86	Q9UL86 homo sapien
21	345	58.9	298	11	Q9QYFO	Q9QYFO mus musculus
22	342	58.4	107	11	Q9ER29	Q9ER29 mus musculus
23	342	58.4	233	11	Q91WS9	Q91WS9 mus musculus
24	340.5	58.1	106	5	Q9U410	Q9U410 schistosoma
25	339	57.8	109	11	Q920E6	Q920E6 mus musculus
26	338.5	57.8	134	11	Q8VDP0	Q8VDP0 mus musculus
27	336.5	57.4	104	11	Q9JL82	Q9JL82 mus musculus
28	333	56.8	108	11	Q8V170	Q8V170 mus musculus
29	330	56.3	116	4	Q96PF6	Q96PF6 homo sapien
30	329	56.1	101	11	Q9JL78	Q9JL78 mus musculus
31	327	55.8	234	11	Q8R028	Q8R028 mus musculus
32	319.5	54.5	235	11	Q91W12	Q91W12 mus musculus
33	316	53.9	97	11	Q9JL76	Q9JL76 mus musculus
34	316	53.9	99	11	Q9JL74	Q9JL74 mus musculus
35	315	53.8	107	11	Q9JL84	Q9JL84 mus musculus
36	313	53.4	218	11	Q92551	Q92551 mus musculus
37	300.5	51.3	241	11	Q921A6	Q921A6 mus musculus
38	300	51.2	127	11	Q92359	Q92359 mus musculus
39	289	49.3	109	6	Q9N0W5	Q9N0W5 oryctolagus
40	255.5	43.6	233	4	Q8YBC9	Q8YBC9 homo sapien
41	238.5	40.7	107	4	Q9NSD6	Q9NSD6 homo sapien
42	236	40.3	107	4	Q9UL82	Q9UL82 homo sapien
43	235.5	40.2	237	4	Q8WUK4	Q8WUK4 homo sapien
44	234.5	40.0	237	4	Q8WTU6	Q8WTU6 homo sapien
45	220.5	37.6	110	4	Q8TE63	Q8TE63 homo sapien

## ALIGNMENTS

RESULT 1					
ID	Q920E9	PRELIMINARY;	PRT;	111	AA.
AC	Q920E9:				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE	Pterin-mimicking anti-Idiotope kappa chain variable region (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Atkin J.D., Tape A., Jennings I.G., Horvath O., Cotton R.G.H.;				
RT	"Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed				
RT	in Mammalian Cells."				
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF307935; AAL09419.1; -				
DR	InterPro; IPR003006; I9_MHC.				
DR	Pfam; PF00047; I9; 1.				
FT	NON_TER	1	1		
FT	NON_TER	111	111		
SQ	SEQUENCE	111	AA;	12046	MM; 1E46988AA6858526 CRC64;
Query Match		80.4%;	Score 471;	DB 11;	Length 111;
Best Local Similarity		81.1%;	Pred. No. 1.9e-45;		
Matches	90;	Conservative	8;	Mismatches	13;
				Indels	0;
				Gaps	0;
QY	1	DIETQSPASLAVSLGQRATISCRASEVSDYGSFWMYQKRGQPKLLIYRASNLDP	60		
DB	1	DIETQSPASLAVSLGQRATISCRASKSVSTGYSYMHYQKRGQPKLLIYASNLDS	60		
QY	61	GIPARSSGSGSDPTLTINPVEDADVATYYCQGSNEDPFTFGSGTKLEIK	111		
DB	61	GVPARSSGSGSDPTLTINPVEEDADVATYYCQHSRELPTTGGGKLEIK	111		

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RESULT 2
O9UL80
ID O9UL80; PRELIMINARY; PRT: 103 AA.
AC O9UL80;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
   (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206026; AAF69324.1; -.
DR HSSP; P80362; 1MTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AB21 CRC64;

Query Match
Best Local Similarity 74.9%; Score 439; DB 11; Length 103;
Matches 83; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

OY 9 ASLAVSLGQRATISCRASESVDSYGHFMQWYQKPGQPKLLIYRASNPFGIPARFSG 68
Db 1 ASLAVSLGQRATISCRASESVDSYGHFMQWYQKPGQPKLLIYRASNPFGIPARFSG 60
OY 69 SSGGTDTLTINVEADVAATYTCQOSNEDPTFGSGTKLEIK 111
Db 61 SSGGTDTLTINHPVEDDIAMFYCOOSRKVPWTEGGCTKLEIK 103

RESULT 3
O9UL77
ID O9UL77; PRELIMINARY; PRT: 108 AA.
AC O9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
```

```
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match
Best Local Similarity 65.9%; Score 386; DB 4; Length 108;
Matches 71; Conservative 20; Mismatches 17; Indels 4; Gaps 1;

OY 1 DIELTQSPASLAVSLGQRATISCRASESVDSYGHFMQWYQKPGQPKLLIYRASNPFG 60
Db 1 DIELTQSPASLAVSLGQRATISCRASESVDSYGHFMQWYQKPGQPKLLIYRASNPFG 56
OY 61 GIPARFSGSGGTDTLTINVEADVAATYTCQOSNEDPTFGSGTKLEIKR 112
Db 57 GIPARFSGSGGTDTLTINVEADVAATYTCQOSNEDPTFGSGTKLEIKR 108

RESULT 4
O9UL70
ID O9UL70; PRELIMINARY; PRT: 108 AA.
AC O9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match
Best Local Similarity 65.4%; Score 383; DB 4; Length 108;
Matches 71; Conservative 19; Mismatches 18; Indels 4; Gaps 1;

OY 1 DIELTQSPASLAVSLGQRATISCRASESVDSYGHFMQWYQKPGQPKLLIYRASNPFG 60
Db 1 DIELTQSPASLAVSLGQRATISCRASESVDSYGHFMQWYQKPGQPKLLIYRASNPFG 56
OY 61 GIPARFSGSGGTDTLTINVEADVAATYTCQOSNEDPTFGSGTKLEIKR 112
Db 57 GIPARFSGSGGTDTLTINVEADVAATYTCQOSNEDPTFGSGTKLEIKR 108

RESULT 5
O96SA9
ID O96SA9; PRELIMINARY; PRT: 107 AA.
AC O96SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
   variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
```

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyreactive monoclonal antibodies from  
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
 RT antibody V region genes."  
 RL J. Immunol. 161:2020-2031(1998).  
 DR EMBL: U96396; AAB68785.1; -  
 DR InterPro: IPR003006; IG\_MHC.  
 DR Pfam: PF00047; Ig\_1.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 64.9%; Score 380.5; DB 4; Length 107;  
 Best Local Similarity 64.3%; Pred. No. 2.9e-35;  
 Matches 72; Conservative 19; Mismatches 16; Indels 5; Gaps 2;

QY 1 DIELOSPASLAVSLGQRTATISCRASESDYSGHSMQWYQKPGQPKLLIYRASNLKP 60  
 DB 1 DIQMOSPSLASVGDRTTICRASQSTISST---LNNYQKPGKAPKLLIYASSTLOS 56  
 QY 61 GIPARFSGSGGDTFTLTINPEADVATYYCOQSNEDPFTGSGTKLEIKR 112  
 DB 57 GVPDRFSGSGGDTFTLTISLQPEDFATYYCOQS-YSTLTFTGGTKVEIKR 107

RESULT 6  
 Q99M37 PRELIMINARY; PRT; 238 AA.

AC 099M37;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Hypothetical 26.3 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC002035; AA02035.1; -  
 DR HSP; P01679; 2EBJ.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR003600; Ig\_1like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig\_2.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; IGc1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00410; IG\_1like; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 64.4%; Score 377.5; DB 11; Length 238;  
 Best Local Similarity 63.7%; Pred. No. 1.8e-34;  
 Matches 72; Conservative 19; Mismatches 21; Indels 1; Gaps 1;

QY 1 DIELOSPASLAVSLGQRTATISCRASES-VDSYSGHSMQWYQKPGQPKLLIYRASNLKP 59  
 DB 20 DVVMOTPTPLSLVSLGDQASISCRSSQSIHNSNGNTYLEMYLQKPGSKLLIYKVSNNP 79  
 QY 60 PCIPARFSGSGGDTFTLTINPEADVATYYCOQSNEDPFTGSGTKLEIKR 112  
 DB 80 SCVPRFSGSGGDTFTLTISLQPEDFATYYCOQS-YSTLTFTGGTKVEIKR 107

RESULT 7  
 Q9UL78 PRELIMINARY; PRT; 109 AA.  
 AC 09UL78;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035036; AAD56272.1; -  
 DR HSP; P80362; 1WTL.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 64.1%; Score 375.5; DB 4; Length 109;  
 Best Local Similarity 65.2%; Pred. No. 1.1e-34;  
 Matches 73; Conservative 15; Mismatches 21; Indels 3; Gaps 1;

QY 1 DIELOSPASLAVSLGQRTATISCRASESDYSGHSMQWYQKPGQPKLLIYRASNLKP 60  
 DB 1 EIVLTSPPTLSLSPERTATISCRASQSVSS---SYLAWYQKPGKAPKLLIYAGSSRAFT 57  
 QY 61 GIPARFSGSGGDTFTLTINPEADVATYYCOQSNEDPFTGSGTKLEIKR 112  
 DB 58 GIPDRFSGSGGDTFTLTISLQPEDCAVYCOQSSPLTFTGGTKVEIKR 109

RESULT 8  
 Q9RIAS PRELIMINARY; PRT; 214 AA.  
 AC 09RIAS;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Kappa light chain of Mab7 (fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wilde K.G., Yu X., Ekrumodoullah A.K.M., Misra S.;  
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
 RT antibody (Mab 7, its light and heavy chains) and construction of a  
 RT single chain antibody (scFv)."  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF152371; AAD40242.1; -  
 DR HSP; P01679; 2FBJ.  
 DR InterPro: IPR003600; Ig\_1like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00410; IG\_1like; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 FT NON\_TER  
 FT NON\_TER





## RESULT 12

091WF8 PRELIMINARY; PRT: 234 AA.  
 AC 091WF8;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Hypothetical 25.9 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=COLON;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC015292; AAH15292.1;  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR001865; Ribosomal\_S2.  
 DR Pfam: PF00047; Ig\_2.  
 DR PROSITE: PS00290; Ig\_MHC; UNKNOWN\_1.  
 DR PROSITE: PS00962; RIBOSOMAL\_S2\_1; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

## Query Match

Best Local Similarity 62.3%; Score 365; DB 11; Length 234;  
 Matches 68; Conservative 19; Mismatches 21; Indels 4; Gaps 1;

QY 1 DIELTQSPASLAVSLGQRATISGRASESVDSYGHSMQWYQKPGQPKLLIYRASNLPP 60  
 DB 21 DIWMTQTSLSLSDRVTISCRASQDISNTR---LNMYYQKPDGCTVKLLIYTSRLYL 76  
 QY 61 GIPARFSGSGGDTFTLTINPEADVATYYCQSNEDPFTFGSGTKLEIKR 112  
 DB 77 GVPFRFSGSGGDTFTLTINPEADVATYYCQSNEDPFTFGSGTKLEIKR 128

## RESULT 13

09UL79 PRELIMINARY; PRT: 108 AA.  
 AC 09UL79;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:98277139; PubMed-9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR HSSP: P01607; IRET.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 FT NON\_TER 1  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 61.8%; Score 362; DB 4; Length 108;  
 Best Local Similarity 61.6%; Pred. No. 3.6e-33;

Matches 69; Conservative 17; Mismatches 22; Indels 4; Gaps 1;

QY 1 DIELTQSPASLAVSLGQRATISGRASESVDSYGHSMQWYQKPGQPKLLIYRASNLPP 60  
 DB 1 DIWMTQTSLSLSDRVTISCRASQDISNTR---LNMYYQKPDGCTVKLLIYTSRLYL 76  
 QY 61 GIPARFSGSGGDTFTLTINPEADVATYYCQSNEDPFTFGSGTKLEIKR 112  
 DB 57 GVPFRFSGSGGDTFTLTINPEADVATYYCQSNEDPFTFGSGTKLEIKR 108

## RESULT 14

08TCD0 PRELIMINARY; PRT: 239 AA.  
 AC 08TCD0;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Hypothetical 26.2 kDa protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LUNG;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC022362; AAH22362.1;  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

## Query Match

Best Local Similarity 61.0%; Score 357.5; DB 4; Length 239;  
 Matches 68; Conservative 19; Mismatches 25; Indels 1; Gaps 1;

QY 1 DIELTQSPASLAVSLGQRATISGRASESVDSYGHSMQWYQKPGQPKLLIYRASNLPP 59  
 DB 21 DVMTQSPSLPLVTLGQPASISCRSTQSLVSGNRYLNMFGQRPQSPRRLLIYKSNND 80  
 QY 60 PGIPARFSGSGGDTFTLTINPEADVATYYCQSNEDPFTFGSGTKLEIKR 112  
 DB 81 SGVPRFSGSGGDTFTLTINPEADVATYYCQSNEDPFTFGSGTKLEIKR 133

## RESULT 15

08VC55 PRELIMINARY; PRT: 239 AA.  
 AC 08VC55;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Hypothetical 26.3 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=COLON;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC021781; AAH21781.1;  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003597; Ig\_C1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_2.  
 DR SMART: SM00409; Ig\_2.  
 DR SMART: SM00407; IGC1; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00290; Ig\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.

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SQ SEQUENCE 239 AA; 26303 MW; C16119CACCA25C337 CRC64;

Query Match	61.0%;	Score 357.5;	DB 11;	Length 239;
Best Local Similarity	60.2%;	Pred No 3	2a-32.	

Matches 68; Conservative 21; Mismatches 23; Indels 1; Gaps 1.

```

OY      1 DIETQSPASLAVSLGQRTATISCASES-VDSYGHSMQWYQKPGQPKRLIYASNLE 59
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      21 DVLITQTPLSFVNIGQASISCKSTKSLNSDGFYIDWYIQKPGQSPQLLIYVSNRF 80

```

```
QY      60 PGIPARFSGSGSGDTFTLTINPVEADVAITYCCQSNEDPFTFGSGTKLEIKR 112
      112 ||||||| : ||| : ||| ||| : ||| |||||||
Db      81 SGVPDRFSGSGSGDTFTLKISRVEAEDGIVYCFQSNHLPYTFGGGTKLEIKR 133
```

db 21 DVVLITQTPLEPVNIGDQASISCKSTKSLNSDGFYYLDWYLQKPGQSPQLLYLVSNRF 80

60 PCIPARFSGSGSTDTLTINPVEADVATYYCQOSNEDPTFGSGTKLEIKR 112

Db 81 SGVPDRFSSGSGTDTLKRVEAEDLGVIYCCFQSNHLPYTFGGGIRLEIKR 133

Search completed: January 13, 2003, 15:12:38  
Job time : 25.3478 secs

Job time : 25.3478 secs

GenCore version 5.1.3  
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OW protein - protein search, using sw model

Run on: January 13, 2003, 15:11:24 ; Search time 7.7913 Seconds  
(without alignments)  
278.890 Million cell updates/sec

Title: US-09-144-886-87  
Perfect score: 586  
Sequence: 1 DIELTQSPASLAVSLGORAT.....QQSNEDPFTGSGTKLEIKR 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

Database : Published\_Applications\_MA:  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEM\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCIT\_NEM\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEM\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US07\_NEM\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEM\_PUB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEM\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586	100.0	112	9	US-09-144-886-87
2	545	93.0	112	9	US-09-144-886-81
3	540	92.2	112	10	US-09-810-502-37
4	537	91.6	112	9	US-09-144-886-86
5	534	91.1	112	9	US-09-144-886-86
6	531	90.6	112	9	US-09-144-886-84
7	527	89.9	112	9	US-09-144-886-85
8	518	88.4	134	10	US-09-881-823-2
9	511	87.2	112	9	US-09-144-886-94
10	507	86.5	112	10	US-09-810-502-36
11	491	83.8	238	9	US-09-903-327A-4
12	489	83.4	132	9	US-09-879-461-2
13	477	81.4	112	9	US-09-144-886-95
14	476	81.2	106	10	US-09-802-077-6
15	476	81.2	106	10	US-09-802-096-6
16	464	79.2	269	12	US-10-027-770-2
17	463	79.0	269	12	US-10-027-770-5
18	461.5	78.8	111	9	US-09-144-886-93
19	461	78.7	131	10	US-09-286-240-2

20	460	78.5	131	9	US-09-879-461-58	Sequence 58, Appl
21	459	78.3	129	10	US-09-839-447A-2	Sequence 2, Appl
22	456	77.8	111	10	US-09-920-171-5	Sequence 5, Appl
23	454	77.5	131	9	US-09-879-461-14	Sequence 14, Appl
24	452	77.1	111	10	US-09-802-077-2	Sequence 2, Appl
25	452	77.1	111	10	US-09-802-096-2	Sequence 2, Appl
26	445	75.6	218	10	US-09-917-410-2	Sequence 2, Appl
27	440.5	75.2	110	9	US-09-974-052-13	Sequence 13, Appl
28	440.5	75.2	110	9	US-09-974-051-13	Sequence 13, Appl
29	436	74.4	114	10	US-09-920-171-10	Sequence 10, Appl
30	436	74.4	218	10	US-09-802-077-9	Sequence 9, Appl
31	436	74.4	218	10	US-09-802-096-9	Sequence 9, Appl
32	436	74.4	218	10	US-09-920-171-13	Sequence 13, Appl
33	434	74.1	114	10	US-09-920-171-9	Sequence 9, Appl
34	431	73.5	111	10	US-09-920-171-6	Sequence 6, Appl
35	430	73.4	114	10	US-09-920-171-8	Sequence 8, Appl
36	430	73.4	218	10	US-09-920-171-15	Sequence 15, Appl
37	430	73.4	218	10	US-09-920-171-17	Sequence 17, Appl
38	430	73.4	218	10	US-09-920-171-19	Sequence 19, Appl
39	430	73.4	218	10	US-09-920-171-24	Sequence 24, Appl
40	430	73.4	248	10	US-09-920-171-22	Sequence 22, Appl
41	430	73.4	248	10	US-09-920-171-23	Sequence 23, Appl
42	407	69.5	111	10	US-09-920-171-7	Sequence 7, Appl
43	399	68.1	112	9	US-09-144-886-89	Sequence 89, Appl
44	397	67.7	108	10	US-09-056-1608-12	Sequence 12, Appl
45	397	67.7	109	10	US-09-811-123-6	Sequence 6, Appl

## ALIGNMENTS

```

RESULT 1
US-09-144-886-87
; Sequence 87, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144, 886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C25 region VL epitope 2
US-09-144-886-87

Query Match      100.0%  Score 586:  DB 9:  Length 112:
Best Local Similarity 100.0%:  Pred. No. 3.3e-37:
Matches 112:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

QY      1 DIELTQSPASLAVSLGORATISCRASESVDSYGHSEFMWYQKPCQPPKLLIYRASNLKP 60
        |||||||
DB      1 DIELTQSPASLAVSLGORATISCRASESVDSYGHSEFMWYQKPCQPPKLLIYRASNLKP 60
        |||||||

QY      61 GIPARFSGSGSTDTLTITNPVEADVATYYCOQSNEDPFTGSGTKLEIKR 112
        |||||||
DB      61 GIPARFSGSGSTDTLTITNPVEADVATYYCOQSNEDPFTGSGTKLEIKR 112
        |||||||

RESULT 2
US-09-144-886-81
; Sequence 81, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D

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APPLICANT: Amersdorfer, Peter  
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
FILE REFERENCE: 2500.117USO  
CURRENT APPLICATION NUMBER: US/09/144,886  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO: 81  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-81

Query Match 93.0%; Score 545; DB 9; Length 112;  
Best Local Similarity 93.8%; Pred. No. 3.5e-34;  
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIETGSPASLAVSLGQRATISCRASESVDSYGHSMQWYQKPGQPKLLIYRASNLTP 60  
DB 1 DIETGSPASLAVSLGQRATISCRASESVDSYGHSMQWYQKPGQPKLLIYRASNLTP 60

QY 61 GIPARFSGSGSDFTLTINPVADVDVATYYCCQSNEDPFTFGSGTKLEIKR 112  
DB 61 GIPARFSGSGSDFTLTINPVADVDVATYYCCQSNEDPFTFGSGTKLEIKR 112

RESULT 3  
US-09-810-502-37  
Sequence 37, Application US/09810502  
Patent No. US20020034765A1  
GENERAL INFORMATION:  
APPLICANT: Padlan, Eduardo A.  
Daugherty, Bruce L.  
Mark, George E.  
TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY  
OF ANTIBODY VARIABLE DOMAINS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/810,502  
FILING DATE: 16-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/905,280  
FILING DATE: 01-Aug-1997  
APPLICATION NUMBER: 08/609,218  
FILING DATE: 01-Mar-1996  
APPLICATION NUMBER: 08/109,187  
FILING DATE: 19-Aug-1993  
APPLICATION NUMBER: 07/702,217  
FILING DATE: 17-May-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hand, J. Mark  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18410CC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720

TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-810-502-37

Query Match 92.2%; Score 540; DB 10; Length 112;  
Best Local Similarity 92.9%; Pred. No. 8.2e-34;  
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIETGSPASLAVSLGQRATISCRASESVDSYGHSMQWYQKPGQPKLLIYRASNLTP 60  
DB 1 DIETGSPASLAVSLGQRATISCRASESVDSYGHSMQWYQKPGQPKLLIYRASNLTP 60

QY 61 GIPARFSGSGSDFTLTINPVADVDVATYYCCQSNEDPFTFGSGTKLEIKR 112  
DB 61 GIPARFSGSGSDFTLTINPVADVDVATYYCCQSNEDPFTFGSGTKLEIKR 112

RESULT 4  
US-09-144-886-80  
Sequence 80, Application US/09144886  
Patent No. US2002015511A1  
GENERAL INFORMATION:  
APPLICANT: Marks, James D  
APPLICANT: Amersdorfer, Peter  
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
FILE REFERENCE: 2500.117USO  
CURRENT APPLICATION NUMBER: US/09/144,886  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO: 80  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-80

Query Match 91.6%; Score 537; DB 9; Length 112;  
Best Local Similarity 92.9%; Pred. No. 1.4e-33;  
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIETGSPASLAVSLGQRATISCRASESVDSYGHSMQWYQKPGQPKLLIYRASNLTP 60  
DB 1 DIETGSPASLAVSLGQRATISCRASESVDSYGHSMQWYQKPGQPKLLIYRASNLTP 60

QY 61 GIPARFSGSGSDFTLTINPVADVDVATYYCCQSNEDPFTFGSGTKLEIKR 112  
DB 61 GIPARFSGSGSDFTLTINPVADVDVATYYCCQSNEDPFTFGSGTKLEIKR 112

RESULT 5  
US-09-144-886-86  
Sequence 86, Application US/09144886  
Patent No. US2002015511A1  
GENERAL INFORMATION:  
APPLICANT: Marks, James D  
APPLICANT: Amersdorfer, Peter  
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
FILE REFERENCE: 2500.117USO  
CURRENT APPLICATION NUMBER: US/09/144,886  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98

;; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98

SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 94  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-94

Query Match  
Best Local Similarity 87.2%; Score 511; DB 9; Length 112;  
Pred. No. 1,1e-31;  
Matches 97; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 IELTQSPASLAVSLGQRATISCRASESYDSYSGHSPQWYQKPGQPKLLIYRASNLSP 61  
DB 2 IELTQSPASLAVSLGQRATISCRASESYDSYSGHSPQWYQKPGQPKLLIYRASNLSP 61

QY 62 IPARFSGSGSGDTFTLTINPEADVAITYCCQSNEDPFTFGSGTKLEIK 111  
DB 62 VPARFSGSGSGDTFTLTINPEADVAITYCCQSNEDPFTFGSGTKLEIK 111

RESULT 10  
US-09-810-502-36  
Sequence 36, Application US/09810502  
Patent No. US20020034765A1  
GENERAL INFORMATION:  
APPLICANT: Padlan, Eduardo A.  
Daugherty, Bruce L.  
Mark, George E.  
TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY  
OF ANTIBODY VARIABLE DOMAINS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/810, 502  
FILING DATE: 16-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/905,280  
FILING DATE: 01-Aug-1997  
APPLICATION NUMBER: 08/609,218  
FILING DATE: 01-Mar-1996  
APPLICATION NUMBER: 08/109,187  
FILING DATE: 19-Aug-1993  
APPLICATION NUMBER: 07/702,217  
FILING DATE: 17-May-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hand, J. Mark  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18410CC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-810-502-36

Query Match  
Best Local Similarity 86.5%; Score 507; DB 10; Length 112;  
Pred. No. 2.2e-31;  
Matches 98; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIELTQSPASLAVSLGQRATISCRASESYDSYSGHSPQWYQKPGQPKLLIYRASNLSP 60  
DB 1 DIYMTQSSNSLAVSLGQRATISCRASESYDSYSGHSPQWYQKPGQPKLLIYRASNLSP 60

QY 61 GIPARFSGSGSGDTFTLTINPEADVAITYCCQSNEDPFTFGSGTKLEIK 112  
DB 61 GIPDRFSGSGSGDTFTLTINPEADVAITYCCQSNEDPFTFGSGTKLEIK 112

RESULT 11  
US-09-903-327A-4  
Sequence 4, Application US/09903327A  
Patent No. US2002016433A1  
GENERAL INFORMATION:  
APPLICANT: Nemetow, Glen R.  
Erguang  
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR  
TITLE OF INVENTION: GENE  
FILE REFERENCE: 22908-1228  
CURRENT APPLICATION NUMBER: US/09/903,327A  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 09/613,017  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Mouse  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (0)...(0)  
OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody  
US-09-903-327A-4

Query Match  
Best Local Similarity 83.8%; Score 491; DB 9; Length 238;  
Pred. No. 6.4e-30;  
Matches 94; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIELTQSPASLAVSLGQRATISCRASESYDSYSGHSPQWYQKPGQPKLLIYRASNLSP 60  
DB 21 DIYLTQSPASLAVSLGQRATISCRASESYDSYSGHSPQWYQKPGQPKLLIYRASNLSP 80

QY 61 GIPARFSGSGSGDTFTLTINPEADVAITYCCQSNEDPFTFGSGTKLEIK 112  
DB 81 GIPARFSGSGSGDTFTLTINPEADVAITYCCQSNEDPFTFGSGTKLEIK 132

RESULT 12  
US-09-879-461-2  
Sequence 2, Application US/09879461  
Publication No. US20020193575A1  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
Gross, Mitchell S.  
Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: Corporate Intellectual Property, UW2220 - 709  
Swedeland Rd.  
CITY: King of Prussia

STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/879,461  
FILING DATE: 12-Jun-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/612,929  
FILING DATE: <unknown>  
APPLICATION NUMBER: US 08/136,783  
FILING DATE: 14-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sulton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-879-461-2  
Query Match 83.4%, Score 489, DB 9, Length 132;  
Best Local Similarity 84.8%, Pred. No. 5.4e-30;  
Matches 95, Conservative 5, Mismatches 12, Indels 0, Gaps 0;  
OY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGOPPKLLITYRASNLPP 60  
DB 21 DIQLTQSPASLAVSLGQRTATISCRASQSDYDGDSDYMMYQKPGOPPKLLITYASNLSS 80  
OY 61 GIPARFSGSGCTDFTLTINPEADVATYYCOQSNEDPFTFGSGTKLEIKR 112  
DB 81 GIPARFSGSGCTDFTLTINHPVEEDATYYCOQSNEDPFTFGSGTKLEIKR 132  
RESULT 13  
US-09-144-886-95  
Sequence 96, Application US/09144886  
Patent No. US20020155114A1  
GENERAL INFORMATION:  
APPLICANT: Marks, James D  
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
TITLE OF INVENTION: Botulinum Neurotoxins  
FILE REFERENCE: P500.117USO  
CURRENT APPLICATION NUMBER: US/09/144,886  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 95  
LENGTH: 112  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-95  
Query Match 81.4%, Score 477, DB 9, Length 112;  
Best Local Similarity 81.2%, Pred. No. 3.6e-29;  
Matches 91, Conservative 8, Mismatches 13, Indels 0, Gaps 0;

OY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGOPPKLLITYRASNLPP 60  
DB 1 DIETQSPASLAVSLGQRTATISCRASESVYEGTLMQWYQKPGOPPKLLITYASNLSS 60  
OY 61 GIPARFSGSGCTDFTLTINPEADVATYYCOQSNEDPFTFGSGTKLEIKR 112  
DB 61 GIPARFSGSGCTDFTLTINHPVEEDATYYCOQSNEDPFTFGSGTKLEIKR 112  
RESULT 14  
US-09-802-077-6  
Sequence 6, Application US/09802077  
Patent No. US20010033842A1  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)  
FILE REFERENCE: P0718P2C2US  
CURRENT APPLICATION NUMBER: US/09/802,077  
CURRENT FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: PCT/US92/06860  
PRIOR FILING DATE: 1992-08-14  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 64  
SEQ ID NO 6  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-802-077-6  
Query Match 81.2%, Score 476, DB 10, Length 106;  
Best Local Similarity 84.9%, Pred. No. 4e-29;  
Matches 90, Conservative 7, Mismatches 9, Indels 0, Gaps 0;  
OY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSMQWYQKPGOPPKLLITYRASNLPP 60  
DB 1 DIQLTQSPASLAVSLGQRTATISCRASQSDYDGDSDYMMYQKPGOPPKLLITYASNLSS 60  
OY 61 GIPARFSGSGCTDFTLTINPEADVATYYCOQSNEDPFTFGSGT 106  
DB 61 GIPARFSGSGCTDFTLTINHPVEEDATYYCOQSNEDPFTFGAGT 106  
RESULT 15  
US-09-802-096-6  
Sequence 6, Application US/09802096  
Patent No. US2001003839A1  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)  
FILE REFERENCE: P0718P2C3US  
CURRENT APPLICATION NUMBER: US/09/802,096  
CURRENT FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: PCT/US92/06860  
PRIOR FILING DATE: 1992-08-14  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 64  
SEQ ID NO 6

; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-802-096-6

Query Match 81.2%; Score 476; DB 10; Length 106;  
Best Local Similarity 84.9%; Pred. No. 4e-29;  
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGORATISCRASESVDSYGHSEFMOWYQOKPGOPPKLLIYRASNLTP 60  
Db 1 DIETOSPASLAVSLGORATISCRASOSVDYDGDSTMMWYQOKPGOPPKLLIYRASNLTP 60  
QY 61 GIPARFSGSGSGTDFTLINPEADDVATYCCOQSNEDPPTFGSGT 106  
Db 61 GIPARFSGSGSGTDFTLINHPVEEDATYCCOQSNEDPPTFGAGT 106

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Job time : 7.7913 secs



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## OM protein - protein search, using sw model

Run on: January 13, 2003, 15:10:24 : Search time 11.2 Seconds  
(without alignments)  
294.229 Million cell updates/sec

Title: US-09-144-886-87

Perfect score: 586

Sequence: 1 DIETQSPASLAVSLGORAT.....QSNEDPFTGSGTKLEIKR 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /cgn2\_6/ptodata/1/1aa/6R.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	525	89.6	131	2	US-08-436-717-33
3	523	89.2	131	2	US-08-621-751A-10
4	522	89.1	149	2	US-08-894-922A-6
5	522	89.1	252	2	US-08-894-922A-14
6	522	89.1	271	2	US-08-894-922A-10
7	518	88.4	120	1	US-08-111-080-26
8	518	88.4	120	1	US-08-211-980-26
9	518	88.4	120	5	PCT-US93-07967-26
10	511	87.2	121	1	US-08-111-080-22
11	511	87.2	121	1	US-08-211-980-22
12	511	87.2	121	5	PCT-US93-07967-22
13	506	86.3	111	1	US-08-275-053-11
14	506	86.3	121	1	US-08-111-080-18
15	506	86.3	121	1	US-08-211-980-18
16	506	86.3	121	5	PCT-US92-07111-17
17	506	86.3	121	5	PCT-US93-07967-18
18	501	85.5	112	3	US-09-065-059-13
19	490	83.6	215	4	US-09-170-769A-4
20	489	83.4	132	2	US-08-483-636-2
21	489	83.4	132	2	US-08-483-636-2
22	481	82.1	111	1	US-08-491-845-8
23	479	81.7	131	4	US-08-579-378A-14
24	476	81.2	106	3	US-08-466-151-6
25	476	81.2	106	4	US-08-466-151-6
26	470	80.2	113	2	US-08-553-497A-6
27	468	79.9	113	2	US-08-553-497A-10

28	465	79.4	111	3	US-08-881-037-76	Sequence 76, Appl
29	464	79.2	106	4	US-09-170-769A-25	Sequence 25, Appl
30	464	79.2	131	1	US-08-137-117D-25	Sequence 25, Appl
31	464	79.2	131	2	US-08-436-717-25	Sequence 25, Appl
32	463	79.0	111	1	US-07-634-278-54	Sequence 54, Appl
33	463	79.0	111	1	US-08-477-728-54	Sequence 54, Appl
34	463	79.0	111	1	US-08-474-040-54	Sequence 54, Appl
35	463	79.0	111	1	US-08-487-200-54	Sequence 54, Appl
36	463	79.0	111	4	US-08-484-537-54	Sequence 54, Appl
37	463	79.0	131	1	US-07-634-278-67	Sequence 67, Appl
38	463	79.0	131	1	US-08-477-728-67	Sequence 67, Appl
39	463	79.0	131	1	US-08-474-040-67	Sequence 67, Appl
40	463	79.0	131	1	US-08-487-200-67	Sequence 67, Appl
41	463	79.0	131	2	US-08-621-751A-14	Sequence 14, Appl
42	463	79.0	131	4	US-08-484-537-67	Sequence 67, Appl
43	462	78.8	120	1	US-08-111-080-24	Sequence 24, Appl
44	462	78.8	120	1	US-08-211-980-24	Sequence 24, Appl
45	462	78.8	120	5	PCT-US93-07967-24	Sequence 24, Appl

## ALIGNMENTS

RESULT 1  
US-08-137-117D-33  
; Sequence 33, Application US/08137117D  
; Patent No. 5795965  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117D  
; FILING DATE: 20-DEC-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP92/00544  
; FILING DATE: 24-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-32084  
; FILING DATE: 19-FEB-1992  
; APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-95476  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25, 258  
; REFERENCE/DOCKET NUMBER: 53466/126/AOAK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-107-117D-33

Query Match 89.6%; Score 525; DB 1; Length 131;  
Best Local Similarity 91.9%; Pred. No. 8.5e-43;  
Matches 102; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DILTOSPASLAVSLGCRATISCRASEVDSYGHSPWQWYQKRGQPKLLIYRASNL6P 60  
DB 21 DYLIOGSPASLAVSLGCRATISCRASEVDSYGHSPWQWYQKRGQPKLLIYRASNL6P 80

QY 61 GIPARESGSGGTFTLTINPVEADVATYYCOQSNEDPPTFGSGTKLEIK 111  
DB 81 GIPARESGSGGTFTLTINPVEADVATYYCOQSNEDPPTFGSGTKLEIK 131

## RESULT 2

US-08-436-717-33

Sequence 33, Application US/08436717  
Patent No. 58177B0

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: SATO, Koh

APPLICANT: BENDIG, Mary

APPLICANT: JONES, Steven

APPLICANT: SALDANHA, Jose

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESS: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,717

FILING DATE:

CLASSIFICATION: 536

Prior Application DATA:

APPLICATION NUMBER: US/08/137,117

FILING DATE: 20-DEC-1993

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 24-APR-1992

Prior Application DATA:

APPLICATION NUMBER: JP 4-32084

FILING DATE: 19-FEB-1992

Prior Application DATA:

APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/126/AAOK

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 131 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-436-717-33

Query Match 89.6%; Score 525; DB 2; Length 131;  
Best Local Similarity 91.9%; Pred. No. 8.5e-43;  
Matches 102; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DILTOSPASLAVSLGCRATISCRASEVDSYGHSPWQWYQKRGQPKLLIYRASNL6P 60  
DB 21 DYLIOGSPASLAVSLGCRATISCRASEVDSYGHSPWQWYQKRGQPKLLIYRASNL6P 80

QY 61 GIPARESGSGGTFTLTINPVEADVATYYCOQSNEDPPTFGSGTKLEIK 111  
DB 81 GIPARESGSGGTFTLTINPVEADVATYYCOQSNEDPPTFGSGTKLEIK 131

## RESULT 3

US-08-621-751A-10

Sequence 10, Application US/08621751A  
Patent No. 5882644

GENERAL INFORMATION:

APPLICANT: Chang, Chung N.

APPLICANT: Landolfi, Nicholas F.

APPLICANT: Martin, Ulrich

TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE

TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESS: MORRISON & FORSTER LLP

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,751A

FILING DATE: 22-MAR-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 321152000100

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141 MRSN FOERS SFO

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 131 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-621-751A-10

Query Match 89.2%; Score 523; DB 2; Length 131;  
Best Local Similarity 91.9%; Pred. No. 1.3e-42;  
Matches 102; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DILTOSPASLAVSLGCRATISCRASEVDSYGHSPWQWYQKRGQPKLLIYRASNL6P 60  
DB 21 DYLIOGSPASLAVSLGCRATISCRASEVDSYGHSPWQWYQKRGQPKLLIYRASNL6P 80

QY 61 GIPARESGSGGTFTLTINPVEADVATYYCOQSNEDPPTFGSGTKLEIK 111  
DB 81 GIPARESGSGGTFTLTINPVEADVATYYCOQSNEDPPTFGSGTKLEIK 131

## RESULT 4

US-08-894-922A-6  
Sequence 6, Application US/08894922A

```
: Patent No. 5863765
: GENERAL INFORMATION:
: APPLICANT: BERRY, Mark John
: APPLICANT: DAVIS, Paul James
: APPLICANT: VAN DER LOOT, Cornelius P.E.
: APPLICANT: WHITELAM, Garry Clark
: TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pillsbury Medison & Sutoro, L.L.P.
: STREET: 1100 New York Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: United States
: ZIP: 20005-3918
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS Word
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/894,922A
: FILING DATE: 03-SEP-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9504344.4
: FILING DATE: 03-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/GB96/00468
: FILING DATE: 01-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Kokulis, Paul K.
: REGISTRATION NUMBER: 16,773
: REFERENCE/DOCKET NUMBER: 60113/241261
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)-861-3503
: TELEFAX: (202)-822-0944
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 149 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-894-922A-6

Query Match      89.1%; Score 522; DB 2; Length 149;
Best Local Similarity 90.4%; Pred. No. 1.9e-42;
Matches 103; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

Oy      1 DIETQSPASLAIVSGORATISCRASESVDSYGFHFMQWYQOKPGOPKLLIYRASNIKP 60
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      23 DIETQSPDSLAVSLGQRTATISCRASESVDSYGFHFMQWYQOKPGOPKLLIYRASNIKS 82

Oy      61 GIPARFSGSGGTDTLTINPEADVATYYCQGSNDP--FTFGSGTKLEIKR 112
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      83 GIPARFSGGTGTDTLTINPEADVATYYCQGSDEYFYMTFGGKLEIKR 136

RESULT 5
US-08-894-922A-14
: Sequence 14, Application US/08894922A
: Patent No. 5863765
: GENERAL INFORMATION:
: APPLICANT: BERRY, Mark John
: APPLICANT: DAVIS, Paul James
: APPLICANT: VAN DER LOOT, Cornelius P.E.
: APPLICANT: WHITELAM, Garry Clark
: TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pillsbury Medison & Sutoro, L.L.P.
: STREET: 1100 New York Avenue, N.W.
: CITY: Washington
```

```
: STATE: D.C.
: COUNTRY: United States
: ZIP: 20005-3918
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS Word
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/894,922A
: FILING DATE: 03-SEP-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9504344.4
: FILING DATE: 03-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/GB96/00468
: FILING DATE: 01-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Kokulis, Paul K.
: REGISTRATION NUMBER: 16,773
: REFERENCE/DOCKET NUMBER: 60113/241261
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)-861-3503
: TELEFAX: (202)-822-0944
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 252 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-894-922A-14

Query Match      89.1%; Score 522; DB 2; Length 252;
Best Local Similarity 90.4%; Pred. No. 3.3e-42;
Matches 103; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

Oy      1 DIETQSPASLAIVSGORATISCRASESVDSYGFHFMQWYQOKPGOPKLLIYRASNIKP 60
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      126 DIETQSPDSLAVSLGQRTATISCRASESVDSYGFHFMQWYQOKPGOPKLLIYRASNIKS 185

Oy      61 GIPARFSGSGGTDTLTINPEADVATYYCQGSNDP--FTFGSGTKLEIKR 112
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      186 GIPARFSGGTGTDTLTINPEADVATYYCQGSDEYFYMTFGGKLEIKR 239

RESULT 6
US-08-894-922A-10
: Sequence 10, Application US/08894922A
: Patent No. 5863765
: GENERAL INFORMATION:
: APPLICANT: BERRY, Mark John
: APPLICANT: DAVIS, Paul James
: APPLICANT: VAN DER LOOT, Cornelius P.E.
: APPLICANT: WHITELAM, Garry Clark
: TITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pillsbury Medison & Sutoro, L.L.P.
: STREET: 1100 New York Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: United States
: ZIP: 20005-3918
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS Word
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/894,922A
: FILING DATE: 03-SEP-1997
: CLASSIFICATION: 435
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9504344.4  
FILING DATE: 03-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB96/00468  
FILING DATE: 01-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Kokulis, Paul K.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 60113/241261  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)-861-3503  
TELEFAX: (202)-822-0944  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 271 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-894-922A-10

Query Match 89.1%; Score 522; DB 2; Length 271;  
Best Local Similarity 90.4%; Pred. No. 3.6e-42;  
Matches 103; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 1 DIETQSPASLAVSLGQRATISCRASEVDYSGHSMQWYQKPGQPKLLIYRASNLEP 60  
DB 145 DIETQSPASLAVSLGQRATISCRASEVDYSGHSMQWYQKPGQPKLLIYRASNLS 204  
QY 61 GIPARFSGSGGTFTLTINPEADVAATYYCOQSNEDPFTFGSGTKLEIKR 112  
DB 205 GIPARFSGSGGTFTLTINPEADVAATYYCOQSNEDPYMYTFGGTKLEIKR 258

## RESULT 7

US-08-111-080-26  
Sequence 26, Application 08/111080  
Patent No. 5558865  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/111,080  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/748,562  
FILING DATE: 22-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-111-080-26

Query Match 88.4%; Score 518; DB 1; Length 120;  
Best Local Similarity 89.3%; Pred. No. 3.6e-42;  
Matches 100; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRATISCRASEVDYSGHSMQWYQKPGQPKLLIYRASNLEP 60  
DB 1 DIETQSPASLAVSLGQRATISCRASEVDYSGHSMQWYQKPGQPKLLIYRASNLS 60

QY 61 GIPARFSGSGGTFTLTINPEADVAATYYCOQSNEDPFTFGSGTKLEIKR 112  
DB 61 GIPARFSGSGGTFTLTINPEADVAATYYCOQSNKDPFTFGAGTKLEIKR 112

## RESULT 8

US-08-211-980-26  
Sequence 26, Application US/08211980  
Patent No. 5665569  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/211,980  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-211-980-26

Query Match 88.4%; Score 518; DB 1; Length 120;  
Best Local Similarity 89.3%; Pred. No. 3.6e-42;

Matches 100; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIETQSPASLAVSLGQATISCRASESVDSYGHSMFYQKPGQPKLLIYRASNLKP 60  
|||  
Db 1 DIVLTQSPASLAVSLGQATISCRASESVDSYGHSMFYQKPGQPKLLIYRASNLKS 60

Qy 61 GIPARFSGSGSTDEFTLTINPEADDAVATYYCOQSNEDPFTGSGTKLEIKR 112  
|||  
Db 61 GIPARFSGSGSTDEFTLTINPEADDAVATYYCOQSNKDPITFGAGTKLEIKR 112

RESULT 9  
PCT-US93-07967-26  
Sequence 26, Application PC/TUS9307967  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07967  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-07967-26

Query Match 88.4%; Score 518; DB 5; Length 120;  
Best Local Similarity 89.3%; Pred. No. 3.6e-42;  
Matches 100; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIETQSPASLAVSLGQATISCRASESVDSYGHSMFYQKPGQPKLLIYRASNLKP 60  
|||  
Db 1 DIVLTQSPASLAVSLGQATISCRASESVDSYGHSMFYQKPGQPKLLIYRASNLKS 60

Qy 61 GIPARFSGSGSTDEFTLTINPEADDAVATYYCOQSNEDPFTGSGTKLEIKR 112  
|||  
Db 61 GIPARFSGSGSTDEFTLTINPEADDAVATYYCOQSNKDPITFGAGTKLEIKR 112

RESULT 10  
US-08-111-080-22  
Sequence 22, Application 08/111080

Patent No. 5558665  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/111,080  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/748,562  
FILING DATE: 22-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-111-080-22

Query Match 87.2%; Score 511; DB 1; Length 121;  
Best Local Similarity 87.5%; Pred. No. 1.6e-41;  
Matches 98; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIETQSPASLAVSLGQATISCRASESVDSYGHSMFYQKPGQPKLLIYRASNLKP 60  
|||  
Db 1 DIVLTQSPASLAVSLGQATISCRASESVDSYGHSMFYQKPGQPKLLIYRASNLKS 60

Qy 61 GIPARFSGSGSTDEFTLTINPEADDAVATYYCOQSNEDPFTGSGTKLEIKR 112  
|||  
Db 61 GIPARFSGSGSTDEFTLTIDPEADDAVATYYCOQNNEDPFTGAGTKLEIKR 112

RESULT 11  
US-08-211-980-22  
Sequence 22, Application US/08211980  
Patent No. 5665569  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago

STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/211,980  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111  
FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-211-980-22

Query Match 87.2%; Score 511; DB 1; Length 121;  
Best Local Similarity 87.5%; Pred. No. 1.6e-41;  
Matches 98; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGGRATISCRASESDYSGHFMQWYQKPGPKLLIYRASNLEP 60  
DB 1 DIVLTOSPASLAVSLGGRATISCRASESDYSGHFMQWYQKPGSPKLLIYVASLTLES 60  
QY 61 GIPARFSGSGGTDFTLTINPEADVDVATYYCOQSNEDPPTFGSGTKLEIKR 112  
DB 61 GVPARFSGSGSRDFTLTIDPEADDAATYYCOQNNEDPLTFGAGTKLEIKR 112

RESULT 12  
PCT-US93-07967-22  
Sequence 22, Application PC/TUS9307967  
GENERAL INFORMATION:  
APPLICANT: Ohno, Tsuneoya  
TITLE OF INVENTION: HIV Immunotherapeutics  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07967  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/07111

FILING DATE: 24-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,457  
FILING DATE: 22-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 31629  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-07967-22

Query Match 87.2%; Score 511; DB 5; Length 121;  
Best Local Similarity 87.5%; Pred. No. 1.6e-41;  
Matches 98; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGGRATISCRASESDYSGHFMQWYQKPGPKLLIYRASNLEP 60  
DB 1 DIVLTOSPASLAVSLGGRATISCRASESDYSGHFMQWYQKPGSPKLLIYVASLTLES 60  
QY 61 GIPARFSGSGGTDFTLTINPEADVDVATYYCOQSNEDPPTFGSGTKLEIKR 112  
DB 61 GVPARFSGSGSRDFTLTIDPEADDAATYYCOQNNEDPLTFGAGTKLEIKR 112

RESULT 13  
US-08-273-053-11  
Sequence 11, Application US/08275053  
Patent No. 5607847  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Recombinant human anti-human immunodeficiency  
virus antibody.  
NUMBER OF SEQUENCES: 16  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/275,053  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/01798  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-273-053-11

Query Match 86.3%; Score 506; DB 1; Length 111;  
Best Local Similarity 87.4%; Pred. No. 4.5e-41;  
Matches 97; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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DB 1 DIVLTOSPASLAVSLGGRATISCRASESDYSGHFMQWYQKPGSPKLLIYVASLTLES 60  
QY 61 GIPARFSGSGGTDFTLTINPEADVDVATYYCOQSNEDPPTFGSGTKLEIKR 111  
DB 61 GVPARFSGSGSRDFTLTIDPEADDAATYYCOQNNEDPLTFGAGTKLEIKR 111

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RESULT 14
US-08-111-080-18
: Sequence 18, Application 08/111080
: Patent No. 5558865
: GENERAL INFORMATION:
: APPLICANT: Ohno, Tsuneya
: TITLE OF INVENTION: HIV Immunotherapeutics
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Borun
: STREET: 6300 Sears Tower, 233 S. Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 08/111,080
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/748,562
: FILING DATE: 22-AUG-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/07111
: FILING DATE: 24-AUG-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/039,457
: FILING DATE: 22-APR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Borun, Michael F.
: REGISTRATION NUMBER: 25,447
: REFERENCE/DOCKET NUMBER: 31629
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3836
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 121 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-111-080-18

Query Match      86.3%; Score 506; DB 1; Length 121;
Best Local Similarity 86.6%; Pred. No. 4.9e-41;
Matches 97; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

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DB 1 DIVLTQSPASLAVSLGQRATISCRASESVDSYGSFWMYQKPGQSPRLIYVASNLES 60

QY 61 GIPARFSGSGSDTFTLTINPVEADDAATYYCOQSNEDPFTGSGTKLEIKR 112
   |||||||
DB 61 GVPARFSGSGSDTFTLTIDPVEADDAATYYCOQNNEDPLAFGTGKLEIKR 112

RESULT 15
US-08-211-980-18
: Sequence 18, Application US/08211980
: Patent No. 5665569
: GENERAL INFORMATION:
: APPLICANT: Ohno, Tsuneya
: TITLE OF INVENTION: HIV Immunotherapeutics
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
```

```
: ADDRESSEE: Borun
: STREET: 6300 Sears Tower, 233 S. Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/211,980
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/07111
: FILING DATE: 24-AUG-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/039,457
: FILING DATE: 22-APR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Borun, Michael F.
: REGISTRATION NUMBER: 25,447
: REFERENCE/DOCKET NUMBER: 31629
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3836
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 121 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-211-980-18

Query Match      86.3%; Score 506; DB 1; Length 121;
Best Local Similarity 86.6%; Pred. No. 4.9e-41;
Matches 97; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIETQSPASLAVSLGQRATISCRASESVDSYGSFWMYQKPGQSPRLIYRASNLEP 60
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DB 1 DIVLTQSPASLAVSLGQRATISCRASESVDSYGSFWMYQKPGQSPRLIYVASNLES 60

QY 61 GIPARFSGSGSDTFTLTINPVEADDAATYYCOQSNEDPFTGSGTKLEIKR 112
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DB 61 GVPARFSGSGSDTFTLTIDPVEADDAATYYCOQNNEDPLAFGTGKLEIKR 112
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Search completed: January 13, 2003, 15:13:43  
Job time : 12.2 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2003, 15:07:08 ; Search time 30.1913 Seconds  
(without alignments)  
494.317 Million cell updates/sec

Title: US-09-144-886-87

Perfect score: 586

Sequence: 1 DIELTQSPASLAIVSLGQRA.....QQSNDDPTFGSGTKLEIKR 112

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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22: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:\*

23: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	544	92.8	249	22	AA20436	Anti-FIX/FIXa anti
2	543	92.7	112	22	AAU07480	Synthetic antibody
3	543	92.7	112	22	AAU07516	Antibody scFv8 lig
4	543	92.7	252	22	AAU07497	Synthetic antibody
5	540	92.2	112	12	AA13089	Murine 1B4 light c
6	540	92.2	112	23	ABB77332	Mouse 1B4 light c
7	533	91.0	111	15	AA147494	Murine anti-CD18 A
8	533	91.0	131	17	AAW01143	Mab 1.4 light chain
9	533	91.0	131	19	AAW41468	Monoclonal antibody
10	529	90.3	294	22	AA20442	Anti-FIX/FIXa anti

11	529	90.3	732	22	AA20437	Anti-FIX/FIXa anti
12	525	89.6	131	13	AA29008	p64-k protein pro
13	525	89.6	325	22	AA20438	Anti-FIX/FIXa anti
14	523	89.2	131	18	AAW30278	Light chain of Mm
15	522	89.1	149	17	AAW02292	FvKc-II VL region.
16	522	89.1	252	17	AAW02294	Yeast-FvKc-II-KEX2
17	522	89.1	271	17	AAW02293	FvKc-II-KEX2. Chl
18	522	89.1	495	22	AA27414	Double-head antibo
19	521	88.9	249	22	AA20435	Anti-FIX/FIXa anti
20	516	88.1	112	16	AA279158	Human IgE receptor
21	515	87.9	120	15	AA248620	Sequence of the 11
22	513	87.5	112	12	AA210539	Chimeric Mab 9.2.2
23	511	87.2	121	17	AAW09259	Monoclonal antibody
24	510	87.0	110	15	AA260810	Light chain variab
25	507	86.5	112	23	ABB77331	Veneered 1B4 light
26	507	86.5	329	22	AA270840	SNV-leader/hum
27	506	86.3	111	16	AA265172	Murine NM-01 varia
28	506	86.3	112	16	AA279156	Human IgE receptor
29	506	86.3	121	17	AAW09274	Mab NM-01 light ch
30	502	85.7	113	22	AA271895	Monoclonal antibody
31	502	85.7	121	15	AA248615	Sequence of the mo
32	501	85.5	112	17	AAW00830	Variable light cha
33	501	85.5	112	18	AAW19016	Anti-human FasL an
34	501	85.5	112	18	AAW27358	Light chain variab
35	499	85.2	121	15	AA248616	Sequence of the mo
36	497	84.8	121	14	AA233466	Sequence of the va
37	495	84.5	132	12	AA210920	Kappa light chain
38	493.5	84.2	132	14	AA237716	Mouse 4C10 anti-Id
39	493	84.1	107	18	AAW27353	Light chain variab
40	493	84.1	112	18	AAW27527	Light chain variab
41	493	84.1	237	20	AAW73873	Human antiFc epsilon
42	493	84.1	240	20	AAW73875	Human antiFc epsilon
43	493	84.1	260	16	AA277617	Anti-C5 Mab N19/8
44	491	83.8	108	22	AAU07496	Synthetic antibody
45	491	83.8	238	23	AA218371	Human penton base

#### ALIGNMENTS

RESULT 1	AA20436	standard; Protein; 249 AA.
ID	AA20436	
XX	21-JUN-2001 (first entry)	
AC	AA20436	
XX	Anti-FIX/FIXa antibody 198/Al scfv.	
DT	Factor IX; FIX; Factor IXa; FIXa; scfv; antibody; procoagulant;	
XX	Factor VIII cofactor; blood coagulation disorder; haemophilia A;	
KW	haemorrhagic diathesis; haemostatic; amidiolytic; therapy; mouse.	
XX		
OS	Chimeric - Mus musculus.	
XX	Chimeric - Synthetic.	
FH	Key	Location/Qualifiers
FT	Protein	1..122
FT		/label= VH
FT	Region	99..111
FT		/label= CDR3
FT	Peptide	123..136
FT		/label= Linker
FT	Protein	137..249
FT		/label= VL
FT	Region	230..238
FT		/label= CDR3
FT	Misc-difference	142
FT		/note= "encoded by ACN"
FT	Misc-difference	224
FT		/note= "encoded by GCN"
FT		
XX		

PN WO200119992-A2.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-EP08936.  
XX  
PR 14-SEP-1999; 99AT-0001576.  
XX  
PA (BAXT ) BAXTER AG.  
XX  
PI Schellfänger F, Kerschbaumer R, Falkner F, Dörner F;  
XX  
DR WPI; 2001-290358/30.  
DR N-PSDB; AAF30726.  
XX  
PT New factor IX/factor IXa antibodies and their derivatives useful for  
PT increasing amiotolytic activity of factor IXa, and for treating blood  
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
PS  
PS Example 10; Fig 17; 138pp; English.  
XX  
XX The present sequence is that of a single chain Fv (scFv) derivative  
CC of antibody 198/A1, comprising the heavy (VH) and light (VL) chain  
CC variable regions of 198/A1 joined by an artificial, flexible linker  
CC peptide. The scFv was obtained by PCR amplification of cDNAs for  
CC 198/A1 VH and VL regions and cloning in vector pDAP2. 198/A1 is  
CC an example of anti-human Factor IX (FIX)/activated Factor IX (Fixa)  
CC antibodies of the invention. Anti-FIX/Fixa and their derivatives,  
CC including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor  
CC activity or FIXa activating activity. Administration leads to an  
CC increase in the procoagulant activity of FIXa, even in the presence  
CC of FVIIIa inhibitors. This allows for rapid blood coagulation even  
CC in the absence of FVIII or FVIIIa, and in the case of FVIII  
CC inhibitor patients. The antibodies and derivatives are used in a  
CC claimed pharmaceutical composition for treating patients with blood  
CC coagulation disorders, especially haemophilia A and haemorrhagic  
CC diathesis.  
XX  
XX Sequence 249 AA:  
SQ  
Query Match 92.8%; Score 544; DB 22; Length 249;  
Best Local Similarity 93.8%; Pred. No. 2.4e-39;  
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DIETOSPASLAVSLGGRATISCRASESDSYGSHFQMWTQKPGOPPKLLIYRASNLMP 60  
DB 138 DIETOSPASLAVSLGGRATISCRASESDSYGSHFQMWTQKPGOPPKLLIYRASNLMP 197  
QY 61 GIRARFSGSGSDFTLTINPVEADVATYYCOOSNEDPFTFGSGYKLEIKR 112  
DB 198 GIRARFSGSGSDFTLTINPVEADVATYYCOOSNEDPFTFGAGTRLEIKR 249  
RESULT 2  
AAU07480  
ID AAU07480 standard; Protein; 112 AA.  
XX  
AC AAU07480;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Synthetic antibody scFv(F8) light chain variable region, VL-F8.  
XX  
XX VL-F8: scFv(F8); antimicrobial; antiviral; cytostatic;  
KW immunomodulatory; antibody; gene therapy; HIV; light chain;  
KW human immunodeficiency virus; tumour; metabolic disorder;  
KW immune disorder; auto-immune disorder.  
XX  
XX Synthetic.  
XX OS  
XX PN WO200149713-A2.  
XX  
XX PD 12-JUL-2001.

XX  
XX 29-DEC-2000; 2000WO-IT00554.  
PF  
XX  
XX 30-DEC-1999; 99IT-RM00803.  
PR  
XX  
XX (CNEI ) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.  
PA (CONS-) SOC CONSORTILE METAPONIUM AGROBIOS SRL.  
XX  
XX Benvenuto E, Franconi R, Desiderio A, Tavladoraki P;  
XX  
DR WPI; 2001-502555/55.  
DR N-PSDB; AAS11886.  
XX  
XX Peptides which are able to confer stability and solubility to an  
PT antibody comprising these peptides, useful for treating pathologies  
PT (e.g. tumour) associated with accumulation of a molecule inside or  
PT outside a human, or animal cell -  
XX  
XX Claim 8; Page 69; 109pp; English.  
PS  
XX  
XX The invention relates to peptides which are able to confer stability and  
CC solubility to an antibody comprising these peptides. The peptides  
CC are especially H-FR1, H-FR2, H-FR3, HFR4, L-FR1, L-FR2, L-FR3 or L-FR4  
CC present within a variable region of an antibody which makes the antibody  
CC soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to  
CC H-FR4 are present within the variable region of the heavy chain of an  
CC antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order  
CC (H-FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and  
CC peptides having the sequences of L-FR1 to L-FR4 are present within  
CC the variable region of the light chain of an antibody, covalently  
CC linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(L-  
CC L-FR2)-(L-CDR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and  
CC polynucleotides (e.g. by gene therapy) are useful for the manufacture  
CC of a medicament for the treatment of pathologies associated with  
CC accumulation of a molecule inside or outside a human, animal cell  
CC or plant cell. The pathologies are infectious (e.g. viral infections such  
CC as HIV, human immunodeficiency virus, infections), tumour, metabolic and  
CC immune (especially auto-immune) pathologies. The present sequence  
CC represents the synthetic antibody scFv(F8), light chain variable region,  
CC VL-F8. This antibody is used as the basis for the design of the  
CC peptides and antibody molecules of the invention.  
XX  
XX Sequence 112 AA:  
SQ  
Query Match 92.7%; Score 543; DB 22; Length 112;  
Best Local Similarity 93.8%; Pred. No. 1.3e-39;  
Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
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DB 1 DIETOSPASLAVSLGGRATISCRASESDSYGSHFQMWTQKPGOPPKLLIYRASNLMP 60  
QY 61 GIRARFSGSGSDFTLTINPVEADVATYYCOOSNEDPFTFGSGYKLEIKR 112  
DB 61 GIRARFSGSGSDFTLTINPVEADVATYYCOOSNEDPFTFGGKLEIKR 112  
RESULT 3  
AAU07516  
ID AAU07516 standard; Peptide; 112 AA.  
XX  
AC AAU07516;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Antibody scFv8 light chain variable region.  
XX  
XX Antimicrobial; antiviral; cytostatic; immunomodulatory;  
KW antibody; gene therapy; HIV; human immunodeficiency virus; tumour;  
KW metabolic disorder; immune disorder; auto-immune disorder; lysosyme;  
KW antibody light chain variable region; scFv8.  
XX  
XX Synthetic.  
XX OS

XX XX WO200149713-A2.  
 XX PN  
 XX OS  
 XX 12-JUL-2001.  
 XX XX  
 XX XX 29-DEC-2000; 2000WO-IT00554.  
 XX PF  
 XX XX 30-DEC-1999; 99IT-RM00803.  
 XX PR  
 XX PA (CNEN ) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.  
 XX PA (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.  
 XX PI Benvenuto E, Franconi R, Desiderio A, Taviadoraki P;  
 XX DR WPI: 2001-502555/55.  
 XX XX  
 XX PT Peptides which are able to confer stability and solubility to an  
 XX PT antibody comprising these peptides, useful for treating pathologies  
 XX PT (e.g. tumour) associated with accumulation of a molecule inside or  
 XX PT outside a human, or animal cell -  
 XX XX  
 XX PS Disclosure: Fig 4; 109pp; English.  
 XX XX  
 XX CC The invention relates to peptides which are able to confer stability and  
 XX CC solubility to an antibody comprising these peptides. The peptides  
 XX CC are especially H-FR1, H-FR2, HF-R3, HF-R4, L-FR1, L-FR2, L-FR3 or L-FR4  
 XX CC present within a variable region of an antibody which makes the antibody  
 XX CC soluble and stable in cytoplasm. Peptides having the sequences of HFRI to  
 XX CC H-FR4 are present within the variable region of the heavy chain of an  
 XX CC antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order  
 XX CC (H-FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and  
 XX CC peptides having the sequences of L-FR1 to L-FR4 are present within  
 XX CC the variable region of the light chain of an antibody, covalently  
 XX CC linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(  
 XX CC L-FR2)-(L-CDR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and  
 XX CC polynucleotides (e.g. by gene therapy) are useful for the manufacture  
 XX CC of a medicament for the treatment of pathologies associated with  
 XX CC accumulation of a molecule inside or outside a human, animal cell  
 XX CC or plant cell. The pathologies are infectious (e.g. viral infections such  
 XX CC as HIV, human immunodeficiency virus, infections), tumour, metabolic and  
 XX CC immune (especially auto-immune) pathologies. The present sequence  
 XX CC represents the antibody scfv8 light chain variable region, used as  
 XX CC a basis for making mutant antibodies.  
 XX CC  
 XX S0 Sequence 112 AA:  
 XX  
 XX Query Match 92.7%; Score 543; DB 22; Length 112;  
 XX Best Local Similarity 93.8%; Pred. No. 1.3e-39;  
 XX Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 XX  
 XX QY 1 DIETLOSPASLAVSLGQRTATISCRASESVDSYGHSPMOWOQKPGQPPKLLIYRASNLPP 60  
 XX DB 1 DIETLOSPASLAVSLGQRTATISCRASESVDSYGHSPMOWOQKPGQPPKLLIYRALNLES 60  
 XX QY 61 GIPARFSGSGSTDFTLTINPYEADVDVATYYCOQSNEDPFTGSGTKLEIKR 112  
 XX DB 61 GIPARFSGSGSTDFTLTINPYEADVDVATYYCOQSNEDPFTGSGTKLEIKR 112  
 XX  
 XX RESULT 4  
 XX AAU07497 standard; Protein: 252 AA.  
 XX ID AAU07497;  
 XX AC AAU07497;  
 XX XX  
 XX DT 24-OCT-2001 (first entry)  
 XX XX  
 XX DE Synthetic antibody scfv(f8).  
 XX XX  
 XX KW Antimicrobial; antiviral; cytostatic;  
 KW Immunomodulatory; antibody; gene therapy; HIV; light chain;  
 KW human immunodeficiency virus; tumour; metabolic disorder;  
 KW immune disorder; auto-immune disorder; scfv(f8);

KW cucumber mosaic virus.  
 XX OS  
 XX Synthetic.  
 XX XX  
 XX Key Location/Qualifiers  
 XX FH 1..125  
 XX FT Protein /label= VH  
 XX FT /note= "Heavy chain variable region"  
 XX FT 126..140  
 XX FT /label= Linker\_peptide  
 XX FT /note= "This peptide is specifically claimed in claim 17"  
 XX FT 141..252  
 XX FT /label= VL  
 XX FT /note= "Light chain variable region"  
 XX FT  
 XX PN WO200149713-A2.  
 XX XX  
 XX PD 12-JUL-2001.  
 XX XX  
 XX XX 29-DEC-2000; 2000WO-IT00554.  
 XX XX  
 XX PE 30-DEC-1999; 99IT-RM00803.  
 XX XX  
 XX PR (CNEN ) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.  
 XX PA (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.  
 XX XX  
 XX PI Benvenuto E, Franconi R, Desiderio A, Taviadoraki P;  
 XX DR WPI: 2001-502555/55.  
 XX DR N-PSDB; AAS11887.  
 XX XX  
 XX PT Peptides which are able to confer stability and solubility to an  
 XX PT antibody comprising these peptides, useful for treating pathologies  
 XX PT (e.g. tumour) associated with accumulation of a molecule inside or  
 XX PT outside a human, or animal cell -  
 XX XX  
 XX PS Example 1; Page 81; 109pp; English.  
 XX XX  
 XX CC The invention relates to peptides which are able to confer stability and  
 XX CC solubility to an antibody comprising these peptides. The peptides  
 XX CC are especially H-FR1, H-FR2, HF-R3, HF-R4, L-FR1, L-FR2, L-FR3 or L-FR4  
 XX CC present within a variable region of an antibody which makes the antibody  
 XX CC soluble and stable in cytoplasm. Peptides having the sequences of HFRI to  
 XX CC H-FR4 are present within the variable region of the heavy chain of an  
 XX CC antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order  
 XX CC (H-FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and  
 XX CC peptides having the sequences of L-FR1 to L-FR4 are present within  
 XX CC the variable region of the light chain of an antibody, covalently  
 XX CC linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(  
 XX CC L-FR2)-(L-CDR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and  
 XX CC polynucleotides (e.g. by gene therapy) are useful for the manufacture  
 XX CC of a medicament for the treatment of pathologies associated with  
 XX CC accumulation of a molecule inside or outside a human, animal cell  
 XX CC or plant cell. The pathologies are infectious (e.g. viral infections such  
 XX CC as HIV, human immunodeficiency virus, infections), tumour, metabolic and  
 XX CC immune (especially auto-immune) pathologies. The present sequence  
 XX CC represents the synthetic antibody scfv(f8) which is used as a basis  
 XX CC for constructing synthetic antibodies incorporating the peptides of the  
 XX CC invention.  
 XX CC  
 XX S0 Sequence 252 AA:  
 XX  
 XX Query Match 92.7%; Score 543; DB 22; Length 252;  
 XX Best Local Similarity 93.8%; Pred. No. 3e-39;  
 XX Matches 105; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 XX  
 XX QY 1 DIETLOSPASLAVSLGQRTATISCRASESVDSYGHSPMOWOQKPGQPPKLLIYRASNLPP 60  
 XX DB 141 DIETLOSPASLAVSLGQRTATISCRASESVDSYGHSPMOWOQKPGQPPKLLIYRALNLES 200  
 XX QY 61 GIPARFSGSGSTDFTLTINPYEADVDVATYYCOQSNEDPFTGSGTKLEIKR 112  
 XX DB 201 GIPARFSGSGSTDFTLTINPYEADVDVATYYCOQSNEDPFTGSGTKLEIKR 252

RESULT 5  
AAR13089  
ID AAR13089 standard; Protein; 112 AA.  
XX  
AC AAR13089;  
XX  
DT 01-OCT-1991 (first entry)  
XX  
DE Murine 1B4 light chain-2 variable region.  
XX  
KW Monoclonal antibody; complementarity determining region; CDR;  
KM Integrin; hybridoma 1B4; protein REI; Gal/Rel; Ig.  
XX  
PN EP438312-A.  
PN EP440351-A.  
XX  
PD 24-JUL-1991.  
XX  
PF 17-JAN-1991; 91EP-0300367.  
XX  
PR 20-DEC-1990; 90US-0627421.  
PR 19-JAN-1990; 90US-0467692.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Law MF, Mark GE, Schmidt JA, Singer II;  
XX  
DR WPI; 1991-216985/30.  
DR N-PSDB; AAO12684.  
XX  
PT New recombinant immunoglobulin(s) reactive with leukocyte CD18  
PT complementarity regions useful in treatment of inflammation  
XX  
PS Disclosure; Fig 25; 77pp; English.  
XX  
CC A recombinant human Ig comprises a human heavy chain framework  
CC and murine CDRs (with the heavy chain framework mutated at sites  
CC near the CDRs); a human light chain framework and murine CDRs.  
CC It has a mean IC50 nearly equal to that of the murine monoclonal  
CC antibody from which the CDRs were derived. It is designated  
CC mutated Gal/Rel. The human Ig is capable of binding to a human  
CC CD18 integrin.  
CC The murine CDRs are obtd. from murine hybridoma 1B4  
CC (ATCC HB 10164). The light chain framework is derived from  
CC human myeloma protein REI (EP-239400).  
CC See also AAO12682-84.  
XX  
SQ Sequence 112 AA:  
XX  
Query Match 92.2%; Score 540; DB 12; Length 112;  
Best Local Similarity 92.9%; Pred. No. 2.4e-39;  
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
XX  
QY 1 DIETGSPASLAVSLGCRATISCRASESVSYGSHFQWYQKPGOPPKLLIRASNLKP 60  
DB 1 DIYLTGSPASLAVSLGCRATISCRASESVSYGSHFQWYQKPGOPPKLLIRASNLKP 60  
XX  
QY 61 GIPARFSGSGSGTFTLTINPVEADVAITYCCQSNEDPFTFGSGTKLEIKR 112  
DB 61 GIPARFSGSGSRDFTLTINPVEADVAITYCCQSNEDPFTFGAGTKLEIKR 112  
XX  
RESULT 6  
AAB77332  
ID AAB77332 standard; Protein; 112 AA.  
XX  
AC AAB77332;  
XX  
DT 17-JUN-2002 (first entry)  
XX

DE Mouse 1B4 light chain variable region SEQ ID NO 37.  
XX  
KM Mouse; human; immunoglobulin; antigenicity; immunogenicity.  
XX  
OS Mus sp.  
XX  
PN US2002034765-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 16-MAR-2001; 2001US-0810502.  
XX  
PR 19-AUG-1993; 93US-0109187.  
PR 01-MAR-1996; 96US-0609218.  
PR 01-AUG-1997; 97US-0905280.  
PR 17-MAY-1991; 91US-0702217.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Daugherty BL, Mark GE, Padlan EA;  
XX  
DR WPI; 2002-338924/37.  
XX  
PT Identifying and replacing immunoglobulin surface amino acid residues  
PT useful for converting the antigenicity of a first mammalian species to  
PT a second mammalian species  
XX  
PS Example 1; Fig 12; 36pp; English.  
XX  
CC The invention relates to identifying differences (1) in mammalian species  
CC specific surface amino acid residues on an immunoglobulin which converts  
CC the antigenicity of a first mammalian species to a second mammalian  
CC species. The new method is used for identifying and replacing  
CC immunoglobulin surface amino acid residues which converts the  
CC antigenicity of a first mammalian species to that of a second mammalian  
CC species. The method simultaneously reduces the immunogenicity and  
CC strictly preserves ligand binding properties. The replacement of exterior  
CC amino acid residues has no effect on the ligand binding properties but  
CC greatly alters immunogenicity. The present sequence is that of a PCR  
CC primer used in the construction of the "venered" 1B4 heavy and light  
CC chain variable regions plus those necessary to fuse the human signal and  
CC intronic sequences onto these variable regions. The present sequence is  
CC that of the mouse 1B4 light chain variable region.  
XX  
SQ Sequence 112 AA:  
XX  
Query Match 92.2%; Score 540; DB 23; Length 112;  
Best Local Similarity 92.9%; Pred. No. 2.4e-39;  
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
XX  
QY 1 DIETGSPASLAVSLGCRATISCRASESVSYGSHFQWYQKPGOPPKLLIRASNLKP 60  
DB 1 DIYLTGSPASLAVSLGCRATISCRASESVSYGSHFQWYQKPGOPPKLLIRASNLKP 60  
XX  
QY 61 GIPARFSGSGSGTFTLTINPVEADVAITYCCQSNEDPFTFGSGTKLEIKR 112  
DB 61 GIPARFSGSGSRDFTLTINPVEADVAITYCCQSNEDPFTFGAGTKLEIKR 112  
XX  
RESULT 7  
AAR47494  
ID AAR47494 standard; Protein; 111 AA.  
XX  
AC AAR47494;  
XX  
DT 06-JUL-1994 (first entry)  
XX  
DE Murine anti-CD18 Ab 60.3 light chain.  
XX  
KW Monoclonal antibody; Mab; heavy chain; light chain;  
KW constant region; variable region; amplification; primer;  
KW polymerase chain reaction; PCR; chimera; Ig;  
KW immunoglobulin; humanised antibody; leucocyte; integrin.

XX Mus sp.  
 OS EP578515-A.  
 XX 12-JAN-1994.  
 XX 24-MAY-1993; 93EP-0401328.  
 XX 26-MAY-1992; 92US-0868233.  
 PR (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;  
 PI WPI; 1994-010334/02.  
 DR N-PSDB; AAQ55002.  
 XX  
 PT Humanised monoclonal antibodies prepn. - using comparative model  
 building, by computer database searching  
 XX  
 PS Disclosure; Page 21; 68pp; English.  
 XX  
 CC A humanised monoclonal antibody corresponding to the murine anti-CD18  
 CC antibody 60.3 was prepared. The variable (V) region sequences from  
 CC both the heavy (H) and light (L) chains were determined from cDNA  
 CC (amplified by PCR) and spliced onto human constant (C) regions,  
 CC resulting in a chimeric 60.3 Ab (1991, kappa). The chimeric Ab was  
 CC expressed in tissue culture (A98.653 mouse myeloma cells, detected  
 CC by ELISA), and examined in binding assays. The results from  
 CC competition and inhibition assays showed that the chimeric Ab was  
 CC as effective as the murine 60.3 MAb. The deduced murine VH and VL  
 CC protein sequences were compared to the protein sequence data base,  
 CC and two human Ig protein sequences were selected to be used as  
 CC templates. A murine 60.3 Fv was modeled according to the deduced  
 CC VH and VL protein sequences. Based on the 60.3 Fv model and the two  
 CC human template sequences selected from the protein data base, a  
 CC humanised Fv was modeled. Construction of the humanised 60.3 was  
 CC done by piecing 5 pairs of complementary oligonucleotides together  
 CC (spanning the entire V region) to form the VH and VL. These were  
 CC then attached onto vectors containing genes for appropriate C regions  
 CC to form humanised Ab (1991, kappa). The humanised proteins were again  
 CC expressed in A98.653 cells and binding assays were done. FACS analyses  
 CC indicated that the humanised Ab recognised cells expressing CD18.  
 CC About a dozen of the humanised 60.3 Ab master wells were transferred  
 CC and assayed for Ig.  
 CC  
 XX  
 SQ Sequence 111 AA;  
 Query Match 91.0%; Score 533; DB 15; Length 111;  
 Best Local Similarity 93.7%; Pred. No. 9.5e-39;  
 Matches 104; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 DIETQSPASLAVSLGQRTATSCRASESVDYSGHFMQYQKPPQPKLLTYRASNLEP 60  
 DB 1 DIVLQSPASLAVSLGQRTATSCRASESVDYSGHFMQYQKPPQPKLLTYRASNLEP 60  
 QY 61 GIPARFSGSGGTDTLTINPEADVATYYCOQSNEDPFTGSGTKLEIK 111  
 DB 61 GIPARFSGSGGTDTLTINPEADVATYYCOQSNEDPFTGSGTKLEIK 111  
 Db 61 GIPARFSGSGGTDTLTINPEADVATYYCOQSNEDPFTGSGTKLEIK 111  
 RESULT 8  
 AA01143  
 ID AA01143 standard; Protein: 131 AA.  
 AC AA01143;  
 XX  
 DT 10-FEB-1997 (first entry)  
 XX  
 DE MAb 1.4 light chain, directed against type II phospholipase A2.  
 XX  
 KW Monoclonal antibody; phospholipase; myocardial infarction;

KW pancreatitis; cerebral infarction; acute kidney failure; colitis;  
 KW chronic rheumatism; adult respiratory distress syndrome;  
 KW cardiac shock; treatment; preclinical testing; disease; hybridoma.  
 XX Mus musculus.  
 OS  
 FH Key Location/Qualifiers  
 FT Binding-site 44..58  
 FT Binding-site /label- CDR 1  
 FT Binding-site 74..80  
 FT Binding-site /label- CDR 2  
 FT Binding-site 113..121  
 FT Binding-site /label- CDR 3  
 XX  
 XX WO9620959-A1.  
 XX 11-JUL-1996.  
 XX  
 XX 27-DEC-1995; 95WO-JP02714.  
 XX 29-DEC-1994; 94JP-0340006.  
 PR (YAMA ) YAMANOCHI PHARM CO LTD.  
 PA Kawauchi Y, Masuho Y, Takasaki J, Yasunaga T;  
 PI WPI; 1996-333946/33.  
 DR N-PSDB; AAT40803.  
 XX  
 PT Monoclonal antibody inhibiting type II phospholipase A2 activity  
 PT for treatment of myocardial and cerebral infarction  
 XX  
 XX Claim 6; Figure 10; 69pp; Japanese.  
 PS  
 XX Monoclonal antibodies which inhibit type II phospholipase A2 are  
 CC useful in the treatment of myocardial infarction, cerebral  
 CC infarction, acute kidney failure, chronic rheumatism, cardiac shock,  
 CC pancreatitis, adult respiratory distress syndrome and colitis. The  
 CC antibodies were generated by immunising Balb/C mice with recombinant  
 CC human type II phospholipase A2. Spleen cells from the mice were  
 CC fused with mouse myeloma P3U1 (P3x63Ag8.01) and the hybridomas  
 CC obtained were screened for phospholipase A2 inhibitory activity.  
 CC Active clones were isolated including 12H5, 1.4 and 10.1. These  
 CC were cultured and the antibody isolated from the culture  
 CC supernatant by precipitation with ammonium sulphate and purification  
 CC on a column of protein A-Sepharose CL4B. Because the antibody acts  
 CC on the primate and mouse forms of enzyme as well as human it is  
 CC particularly suitable for preclinical testing.  
 CC  
 XX  
 SQ Sequence 131 AA;  
 Query Match 91.0%; Score 533; DB 17; Length 131;  
 Best Local Similarity 93.7%; Pred. No. 1.1e-38;  
 Matches 104; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DIETQSPASLAVSLGQRTATSCRASESVDYSGHFMQYQKPPQPKLLTYRASNLEP 60  
 DB 21 DIVLQSPASLAVSLGQRTATSCRASESVDYSGHFMQYQKPPQPKLLTYRASNLEP 80  
 QY 61 GIPARFSGSGGTDTLTINPEADVATYYCOQSNEDPFTGSGTKLEIK 111  
 DB 61 GIPARFSGSGGTDTLTINPEADVATYYCOQSNEDPFTGSGTKLEIK 111  
 Db 81 GIPARFSGSGGTDTLTINPEADVATYYCOQSNEDPFTGSGTKLEIK 131  
 RESULT 9  
 AA04168  
 ID AA04168 standard; Protein: 131 AA.  
 AC AA04168;  
 XX  
 DT 16-JUN-1998 (first entry)  
 XX  
 DE Monoclonal antibody 1.4 light chain against type II phospholipase A2.

XX Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin;  
 KW amelioration; kidney disorder; nephrotoxicity; anticancer.  
 XX Unidentified.  
 XX WO9749427-A1.  
 XX 31-DEC-1997.  
 PD 27-JUN-1997; 97WO-JP02241.  
 XX 19-SEP-1996; 96JP-0247635.  
 PR 27-JUN-1996; 96JP-0167286.  
 XX (YAMA ) YAMANOUCHI PHARM CO LTD.  
 PA Hayashi K, Kawachi Y, Masuno Y, Takasaki J;  
 PI WPI: 1998-076914/07.  
 DR N-PSDB: AAV12260.  
 XX Amelioration of kidney disorders caused by cisplatin administration  
 PT - by treatment with an antibody inhibiting type II phospholipase A2  
 PT activity  
 PS Disclosure: Page 35-36; 74pp; Japanese.  
 XX The present sequence represents the monoclonal antibody 1.4 light chain  
 CC against type II phospholipase A2, from the present invention. The  
 CC present invention describes a novel method for the amelioration of  
 CC kidney disorders (such as acute renal failure) associated with the  
 CC administration of cisplatin for the treatment of cancer. The method  
 CC comprises treatment with a monoclonal antibody which inhibits the  
 CC activity of type II phospholipase A2 (particularly of type II  
 CC phospholipase A2 of human origin), or with a protein or peptide  
 CC possessing the same inhibitory activity and containing a part of the  
 CC antibody sequence. Preferably the antibody also inhibits the activity of  
 CC ape and/or mouse type II phospholipase A2, and has the ability to  
 CC release type II phospholipase A2 bound to a cell membrane. Three  
 CC specific monoclonal antibodies having these properties which can be  
 CC used are 12H5, 10.1 and 1.4, derived from hybridomas FERM BP-5300,  
 CC FERM BP-5298 and FERM BP-5297 respectively. The method can be used for  
 CC suppressing the nephrotoxicity which is a characteristic feature of  
 CC cisplatin administration, and therefore allowing more efficient use of  
 CC this drug as an anticancer agent, e.g. by allowing an increased dosage  
 CC to be used.  
 XX Sequence 131 AA;  
 SQ  
 Query Match 91.0%; Score 533; DB 19; Length 131;  
 Best Local Similarity 93.7%; Pred. No. 1,1e-38;  
 Matches 104; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 OY 1 DIETQSPSLAVSLGQRTISCRASESVSYGHSFMWYQKPGQPKLLIYRASNLEP 60  
 DB 21 DIYLGQSPSLAVSLGQRTISCRASESVSYGHSFMWYQKPGQPKLLIYRASNLEP 80  
 OY 61 GIPARFSGSGSTDTLTITNPVEADVAITYYCOQSNEDPFTGSGKLEIK 111  
 DB 81 GIPARFSGSGSTDTLTITNPVEADVAITYYCOQSNEDPFTGSGKLEIK 131  
 RESULT 10  
 AAB20442  
 ID AAB20442 standard; Protein; 294 AA.  
 XX AAB20442;  
 AC AAB20442;  
 XX 21-JUN-2001 (first entry)  
 DT Antl-FIX/FIXa antibody 198/BI-myc-tag fusion.  
 DE  
 XX

KW Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;  
 KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;  
 KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;  
 KW myc-tag.  
 XX Chimeric - Mus musculus.  
 OS Chimeric - Synthetic.  
 OS Chimeric - Escherichia coli.  
 XX Key  
 FT Location/Qualifiers  
 FT 1..22  
 FT /label= Signal\_peptide  
 FT 23..294  
 FT /label= Mature\_protein  
 FT 23..271  
 FT /label= scFv  
 FT 23..144  
 FT /label= VH  
 FT Misc-difference 76  
 FT /note= "encoded by GGN"  
 FT Peptide 145..159  
 FT /label= Linker  
 FT Region 160..271  
 FT /label= VL  
 FT Peptide 272..274  
 FT /label= Spacer  
 FT Protein 275..286  
 FT /label= Myc\_tag  
 FT Peptide 287..288  
 FT /label= Spacer  
 FT Peptide 289..294  
 FT /label= His\_tag  
 PN WO200119992-A2.  
 XX 22-MAR-2001.  
 PD 13-SEP-2000; 2000WO-EP08936.  
 PF 14-SEP-1999; 99AT-0001576.  
 PR (BAXT ) BAXTER AG.  
 PA Schefflinger F, Kerschbaumer R, Falkner F, Dorner F;  
 PI WPI: 2001-290358/30.  
 DR N-PSDB: AAF30732.  
 XX New factor IX/factor IXa antibodies and their derivatives useful for  
 PT increasing amidolytic activity of factor IXa, and for treating blood  
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 PT Example 16; Fig 34; 138pp; English.  
 PS  
 XX The present sequence is that of a fusion protein comprising: a pelb  
 CC leader; a single chain Fv (scFv) derivative of antibody 198/BI  
 CC comprising the heavy (VH) and light (VL) chain variable regions of  
 CC 198/BI joined by an artificial, flexible linker peptide; a spacer;  
 CC a myc-tag peptide; a spacer; and a C-terminal 6His affinity tail.  
 CC 198/BI is an example of anti-human factor IX (FIX)/activated Factor  
 CC IX (FIXa) antibodies of the invention. Anti-FIX/FIXa antibodies and  
 CC their derivatives, including scFv fragments, have FVIIIa cofactor  
 CC activity or FIXa activating activity. Administration leads to an  
 CC increase in the procoagulant activity of FIXa, even in the presence  
 CC of FVIIIa inhibitors. This allows for rapid blood coagulation even  
 CC in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor  
 CC patients. The antibodies and derivatives are used in a claimed  
 CC pharmaceutical composition for treating patients with blood  
 CC coagulation disorders, especially haemophilia A and haemorrhagic  
 CC diathesis. The scFv-myc-tag fusion was expressed in E. coli. It  
 CC exhibited FVIII-like activity.  
 XX Sequence 294 AA;  
 SQ

```

xx      Example 16; Fig 26; 138pp; English.
ps
cc      The present sequence is that of a fusion protein comprising: a PelB
cc      leader; a single chain Fv (scfv) derivative of antibody 198/B1
cc      comprising the heavy (VH) and light (VL) chain variable regions of
cc      198/B1 joined by an artificial, flexible linker peptide; a spacer;
cc      Escherichia coli alkaline phosphatase; and a C-terminal 6His
cc      affinity tail. 198/B1 is an example of anti-human Factor IX
cc      (FIX)/activated Factor IX (FIXa) antibodies of the invention.
cc      Anti-FIX/FIXa antibodies and their derivatives, including scFv
cc      fragments, have FVIII cofactor activity or FIXa activating
cc      activity. Administration leads to an increase in the procoagulant
cc      activity of FIXa, even in the presence of FVIIa inhibitors. This
cc      allows for rapid blood coagulation even in the absence of FVIII or
cc      FIXa, and in the case of FVIII inhibitor patients. The
cc      antibodies and derivatives are used in a claimed pharmaceutical
cc      composition for treating patients with blood coagulation disorders,
cc      especially haemophilia A and haemorrhagic diatheses. The
cc      scfv-alkaline phosphatase was expressed in E. coli. It exhibited
cc      FVIII-like activity.
cc      xx
sq      Sequence    732 AA;
          Query Match           90.3%; Score 529; DB 22; Length 732;
          Best Local Similarity   91.1%; Pred. No. 1,4e-37;
          Matches 102; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Oy      1 DIELIQSPASILAVSLGQKATISCRASESVDSYSGHSFMOWOOKPGOPKLLIYRASNLKP 60
Db      160 DIVLTQSFAASLAVSAGQKATISCRASESVDSYGIVFMHMYYQDIIPQPKLLIYRASNLKS 219
Oy      61 GIPIAFSSGSGCTDETLTINPYEADVAITYYCQGSNEDPFTFGSGTKLEIKR 112
Db      220 GIPIAFSSGSGSRTPDTLTINPYEADDAITYYCQGSNEDPLTFGTGRLEIKR 271
RESULT 12
AAR29008
AAID AAR29008 standard; Protein; 131 AA.
AC AAR29008;
XX 30-MAR-1993 (first entry)
XX p64-k4 protein product.
XX DE
XX Human: antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
KN plasmid; p64-k4; p64-h2.
XX OS
XX Synthetic.
OS
XX Key Location/Qualifiers
XX Peptide 1..20
XX FT /note= "Signal peptide"
XX Protein 21..131
XX FT /note= "Mature peptide"
XX
PM WO9219759-A.
XX PD
XX 12-NOV-1992.
XX PF
XX 24-APR-1992; 92WO-JP00544.
XX PR 25-APR-1991; 91JP-0095476.
XX PR 19-FEB-1992; 92JP-0032084.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WPI: 1992-398882/48.
```

DR N-PSDB; AAO30757.  
 XX Reconstituted human antibody to human interleukin-6 receptor -  
 PT has low antigenicity and contains mouse V-region complementarity  
 PT determining regions  
 XX  
 PS Disclosure; Page 124-125; 207pp; Japanese.  
 CC  
 CC The sequences given in AAR29008-09 were encoded by plasmids which were  
 CC used in example to illustrate the production of a human antibody which  
 CC recognises human interleukin-6 receptor (IL-6R). The antibody  
 CC comprises light (L) chain and heavy (H) chain variable regions which  
 CC were derived from a mouse monoclonal antibody produced from the  
 CC hybridoma AUK64-7 which contained the plasmids p64-K4 and p64-h2.  
 CC  
 XX  
 SQ Sequence 131 AA;  
 Query Match 89.6%; Score 525; DB 13; Length 131;  
 Best Local Similarity 91.9%; Pred. No. 5.5e-38;  
 Matches 102; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 DIETQSPASISAVLSGQRATISCRASESDYSGHSFQMOWQKRGQPKLLIRASMLEP 60  
 DB 21 DIVLTQSPASISAVLSGQRATISCRASESDYSGHSFQMOWQKRGQPKLLIRASMLE 80  
 QY 61 GIPARFSGSGSTFTLTINPVEADVATYYCOQSNEDPFTFGSGTKLEIK 111  
 DB 81 GIPARFSGSGSRDFTLTINPVEADVATYYCOQSNEDPFTFGAGTKLEIK 131  
 RESULT 13  
 AAB20438  
 ID AAB20438 standard; Protein; 325 AA.  
 XX  
 AC AAB20438;  
 XX  
 DT 21-JUN-2001 (first entry)  
 XX  
 DE Anti-Fix/FixA antibody 198/B1 bivalent miniantibody.  
 XX  
 XX Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;  
 KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;  
 KW haemorrhagic diathesis; haemostatic; amido-lytic; therapy; mouse;  
 KW bivalent antibody; plasmid pzip-198AB2#102.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Synthetic.  
 OS Chimeric - Escherichia coli.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..22  
 FT /label= Signal\_peptide  
 FT /note= "Peib leader"  
 FT Protein 23..325  
 FT /label= Mature\_protein  
 FT Protein 23..271  
 FT /label= scfv  
 FT Region 23..144  
 FT /label= VH  
 FT Misc-difference 76  
 FT /note= "encoded by GGN"  
 FT Peptide 145..159  
 FT /label= Linker  
 FT Region 160..271  
 FT /label= VL  
 FT Misc-difference 166  
 FT /note= "encoded by TNM"  
 FT Misc-difference 181  
 FT /note= "encoded by TCN"  
 FT Peptide 272..274  
 FT /label= Spacer  
 FT Protein 275..284  
 FT /label= Hinge

FT Protein 285..319  
 FT /label= Helix  
 FT Peptide 320..325  
 FT /label= His\_tag  
 XX  
 PN WO200119992-A2.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 13-SEP-2000; 2000MO-EP08936.  
 XX  
 PR 14-SEP-1999; 99AT-0001576.  
 XX  
 PA (BAXT ) BAXTER AG.  
 XX  
 PI Scheifflinger F, Kerschbaumer R, Falkner F, Dörner F;  
 DR WPI; 2001-290358/30.  
 DR N-PSDB; AAF30728.  
 XX  
 PT New factor IX/factor IXa antibodies and their derivatives useful for  
 PT increasing amidolytic activity of factor IXa, and for treating blood  
 PT coagulation disorders such as haemophilia A and haemorrhagic diathesis  
 XX  
 PS Example 16; Fig 28; 138pp; English.  
 CC  
 CC The present sequence is that of a bivalent miniantibody comprising  
 CC a Peib leader peptide, the single chain Fv (scfv) fragment of  
 CC antibody 198/B1 (subclone AB2), an amphipathic helical structure  
 CC and a C-terminal 6His tag. The protein was expressed in  
 CC Escherichia coli from plasmid pzip198AB2#102 (see AAF30728).  
 CC Antibody 198/B1 is an example of anti-human Factor IX  
 CC (FIX)/activated Factor IX (FIXa) antibodies of the invention.  
 CC Anti-Fix/FixA antibodies and their derivatives have FVIII cofactor  
 CC activity or FIXa activating activity. Administration leads to an  
 CC increase in the procoagulant activity of FIXa, even in the presence  
 CC of FVIII inhibitors. This allows for rapid blood coagulation even  
 CC in the absence of FVIII or FVIIIa, and in the case of FVIII  
 CC inhibitor patients. The antibodies and derivatives are used in a  
 CC claimed pharmaceutical composition for treating patients with blood  
 CC coagulation disorders, especially haemophilia A and haemorrhagic  
 CC diathesis. The bivalent miniantibody exhibited FVIII-like  
 CC activity.  
 XX  
 SQ Sequence 325 AA;  
 Query Match 89.6%; Score 525; DB 22; Length 325;  
 Best Local Similarity 90.2%; Pred. No. 1.4e-37;  
 Matches 101; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 DIETQSPASISAVLSGQRATISCRASESDYSGHSFQMOWQKRGQPKLLIRASMLEP 60  
 DB 160 DIVLTQSPASISAVLSGQRATISCRASESDYSGHSFQMOWQKRGQPKLLIRASMLE 219  
 QY 61 GIPARFSGSGSTFTLTINPVEADVATYYCOQSNEDPFTFGSGTKLEIK 112  
 DB 220 GIPARFSGSGSRDFTLTINPVEADVATYYCOQSNEDPFTFGTKLEIK 271  
 RESULT 14  
 AAW30278  
 ID AAW30278 standard; Protein; 131 AA.  
 XX  
 AC AAW30278;  
 XX  
 DT 07-JUL-1998 (first entry)  
 XX  
 DE Light chain of MUM4TS.11.  
 XX  
 XX MUM4TS.11; antibody; platelet; beta receptor; PDGF-R beta; inhibition;  
 KW intrinsic hyperplasia; vasculature; restenosis; angioplasty; light chain.  
 XX  
 OS Mus sp.



```

XX Key Location/Qualifiers
FH Protein 20..131
FT /note= "Mature protein"
FT Binding-site 43..58
FT /note= "Complementarity determining region 1"
FT Binding-site 73..80
FT /note= "Complementarity determining region 2"
FT Binding-site 112..120
FT /note= "Complementarity determining region 3"
XX
XX WO9737029-A1.
XX
XX 09-OCT-1997.
XX
XX 19-MAR-1997; 97WO-US04198.
XX
XX 22-MAR-1996; 96US-0621751.
XX
XX (BOE ) BOEHRINGER MANNHEIM GMBH.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Chang CN, Landolfi NF, Martin U;
XX
XX MPI; 1997-503114/46.
XX N-PSDB; AAT90985.
XX
XX Antibodies to platelet derived growth factor beta receptor - inhibit
XX PDGF BB-induced proliferation of cells expressing the receptor, used
XX particularly for inhibiting intimal hyperplasia
XX
XX Claim 11; Fig 7B; 87pp; English.
XX
XX This is the amino acid sequence for the light chain of muM4TS.11, a
XX novel antibody which specifically binds to the platelet derived
XX growth beta receptor (PDGF-R beta), but not within the fifth
XX extracellular Ig-like domain, where the antibody inhibits PDGF
XX BB-induced proliferation of a cell expressing the PDGF beta receptor.
XX The antibody can be used in a method of inhibiting intimal hyperplasia
XX in the vasculature of a mammal. The antibodies can be used for the
XX treatment of disorders related to PDGF activity such as disorders
XX involving proliferation of smooth muscle cells, and including
XX restenosis following angioplasty.
XX
XX Sequence 131 AA:
SQ
XX
XX Query Match 89.2%; Score 523; DB 18; Length 131;
XX Best Local Similarity 91.9%; Pred. No. 8.2e-38;
XX Matches 102; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 1 DIELTQSPASLAVSLGQRATISCRASESVDSYGHSPMOWYQKPGQPKLLIYRASNLSP 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX DB 21 DVLVQSPSLAVSLGQRATISCRASESVDSYGHSPMOWYQKPGQPKLLIYRASNLSP 80
XX
XX QY 61 GIPARFSGSGGTDFTLTINPVEADVDVATYYCOQSNEDPFTFGSGTKLEIKR 111
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX DB 81 GIPARFSGSGGSRDFTLTINPVEADVDVATYYCOQSNEDPFTFGSGTKLEIKR 131
XX
XX RESULT 15
XX AAM02292
XX ID AAM02292 standard: Protein; 149 AA.
XX
XX AAM02292;
XX
XX 22-NOV-1996 (first entry)
XX
XX FVKC-II VL region.
XX
XX Single chain antibody; Fv; FVKC; heavy chain; light chain;
XX antibody engineering; peptide hormone; Pichia pastoris.
XX
XX Mus musculus.

```

```

XX Key Location/Qualifiers
FH Peptide 1..22
FT /label= Pe1B_leader
FT Protein 23..136
FT /label= VLKC
FT Peptide 137..149
FT /label= HydropH11-II
FT /note= "HydropH11 II tag used to facilitate assay of Fv activity"
XX
XX WO9627612-A1.
XX
XX 12-SEP-1996.
XX
XX 01-MAR-1996; 96WO-GB00468.
XX
XX 03-MAR-1995; 95GB-0004344.
XX
XX (UNIL ) QUEST INT BV.
XX
XX Berry MJ, Davis PJ, Van Der Logt CPE, Whitelam GC;
XX
XX MPI; 1996-425380/42.
XX N-PSDB; AAT36906.
XX
XX prodn. of antibody fragments, partic. in yeast - by prodn. of heavy
XX and light chains linked by sequence cleavable by host enzyme
XX
XX Disclosure; Fig 8; 53pp; English.
XX
XX FVKC VH (AAM02291) and VL (AAM02292) chains are encoded by a DNA
XX construct (AAT36906) assembled in E. coli vector pUC19. FVKC
XX is a single-chain antibody that shows specificity for a peptide
XX hormone. Novel antibody fragments (see also AAM02293-94) have
XX been constructed in which the FVKC VH and VL chains are separated
XX by a KEX2-type processing sites, allowing prodn. in yeast, partic.
XX Pichia pastoris, host cells.
XX
XX Sequence 149 AA:
SQ
XX
XX Query Match 89.1%; Score 522; DB 17; Length 149;
XX Best Local Similarity 90.4%; Pred. No. 1.1e-37;
XX Matches 103; Conservative 4; Mismatches 5; Indels 2; Gaps 1;
XX
XX QY 1 DIELTQSPASLAVSLGQRATISCRASESVDSYGHSPMOWYQKPGQPKLLIYRASNLSP 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX DB 23 DIELTQSPSLAVSLGQRATISCRASESVDSYGHSPMOWYQKPGQPKLLIYRASNLSP 82
XX
XX QY 61 GIPARFSGSGGTDFTLTINPVEADVDVATYYCOQSNEDP--FTFGSGTKLEIKR 112
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX DB 83 GIPARFSGSGSRDFTLTINPVEADVDVATYYCOQSNEDPYMYTFGGGTKLEIKR 136
XX
XX Search completed: January 13, 2003, 15:11:18
XX Job time : 31.1913 secs

```



Gencore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:09:39 : Search time 25.6522 Seconds

(without alignments)  
947.817 Million cell updates/sec

Title: US-09-144-886-63

Perfect score: 633  
Sequence: 1 QVQLQESGGGLVPRGSLKLT.....YRYDAMDYWGCGTIVTVSS 118

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Listing first 45 summaries

SPTREMBL\_21:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_ricent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	532	84.0	119	11	Q99KA4
2	515.5	81.4	119	11	Q920E7
3	471	74.4	119	11	Q91205
4	455.5	72.0	119	11	Q91207
5	449.5	71.0	119	11	Q91207
6	446.5	70.5	119	11	Q91207
7	442	69.8	119	11	Q91207
8	433	68.4	119	11	Q91207
9	431	68.1	119	11	Q91207
10	430.5	68.0	119	11	Q91207
11	430	67.9	119	11	Q91207
12	429.5	67.9	121	4	Q9UL71
13	427	67.5	121	4	Q9UL71
14	425	67.1	121	4	Q9UL71
15	424.5	67.1	121	4	Q9UL71
16	424	67.0	121	4	Q9UL71

17	421	66.5	118	4	Q9UL72
18	420.5	66.4	116	4	Q9UL93
19	407	64.3	147	4	Q9Y509
20	406	64.1	298	11	Q9Y509
21	402	63.5	122	4	Q9UL84
22	394	62.2	95	4	Q9ULB6
23	385	60.8	469	11	Q9R3V9
24	380.5	60.1	131	4	Q9UL88
25	366	57.8	484	11	Q9VEA0
26	357	56.4	143	11	Q924P9
27	355	56.1	145	11	Q924R4
28	353.5	55.8	473	11	Q9DBL4
29	352.5	55.7	117	11	Q9DXE9
30	352	55.6	143	11	Q924R0
31	347	54.8	124	4	Q9UL92
32	346.5	54.7	146	11	Q924Q3
33	342	54.0	145	11	Q924R1
34	342	54.0	145	11	Q924O7
35	341.5	53.9	142	11	Q924O1
36	340.5	53.8	142	11	Q924O2
37	338.5	53.5	117	11	Q9OXF0
38	336.5	53.2	146	11	Q924R8
39	336	53.1	143	11	Q924P6
40	335	52.9	145	11	Q924O6
41	334.5	52.8	104	4	Q9UL87
42	334.5	52.8	119	5	Q9GYZ2
43	333	52.6	145	11	Q924O9
44	332	52.4	137	11	Q924R6
45	331.5	52.4	468	11	Q99L31

## ALIGNMENTS

RESULT 1	Q99KA4	PRELIMINARY:	PRT:	487 AA.
ID	Q99KA4			
AC	Q99KA4			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Hypothetical 52.6 kDa protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: BC004786; AA04786.1; -			
DR	HSSP: P01810; 2FBJ.			
DR	InterPro: IPR003599; Ig.			
DR	InterPro: IPR003597; Ig_c1.			
DR	InterPro: IPR003600; Ig_Like.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_v.			
DR	Pfam: PF00047; Ig_4.			
DR	SMART: SM00409; IG: 3.			
DR	SMART: SM00407; IG1: 3.			
DR	SMART: SM00406; IGv: 1.			
DR	SMART: SM00410; IG_Like: 1.			
DR	PROSITE: PS00290; IG_MHC; UNKNOWN_2.			
DR	Hypothetical protein.			
SQ	SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;			
Query Match	84.0%;	Score 532;	DB 11;	Length 487;
Best Local Similarity	83.1%;	Pred. No. 7.6e-45;		
Matches 103;	Conservative 4;	Mismatches 11;	Indels 6;	Gaps 1;
QY	1 QVQLQESGGGLVPRGSLKLTCAASGFTFSDYVYWRKTPERKLEWVAFTISGGSVTVV 60			
DB	20 EVQLVESGGGLVPRGSLKLTCAASGFTFSSYMSWVRTPERKLEWVAFTISGGSVTVV 79			

QY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEPTAMYYCSR-----YRYPDAMDYWGCGTTV 114  
DB 80 PDNVKGRFTISRDNKNNLYLQMSLSKSEPTAMYYCARDMGSGPRGGISRPDIWGCGTTI 139  
QY 115 TVSS 118  
DB 140 TVSS 143

RESULT 2  
Q920E7 PRELIMINARY; PRT; 119 AA.  
AC Q920E7;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
DE Pterin-mimicking anti-idiotope heavy chain variable region  
DE (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.:  
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed  
RT in Mammalian Cells".  
RL Submitted (Sep-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF307932; AL09421.1; -  
DR InterPro: IPR003006; I9\_MHC.  
DR Pfam: PF00047; I9; 1.  
FT NON\_TER  
FT NON\_TER  
SQ SEQUENCE 119 AA; 13025 MW; F6E90404381CA7C CRC64;

Query Match 81.4%; Score 515.5; DB 11; Length 119;  
Best Local Similarity 84.0%; Pred. No. 6e-44;  
Matches 100; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVOLOESGGGLVKKPGSGSLKSCASGFTFSYVWVWQPEKRLLEVAVATISDGSSTYY 60  
DB 1 EVQLVESGGGLVKKPGSGSLKSCASGFTFSYVWVWQPEKRLLEVAVATISDGSSTYY 60  
QY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEPTAMYYCSR--RYDDAMDYWGCGTTVTVSS 118  
DB 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEPTAMYYCARDMGSGPRGGISRPDIWGCGTTI 139

RESULT 3  
Q91205 PRELIMINARY; PRT; 473 AA.  
AC Q91205;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Hypothetical 51.9 kDa protein.  
GN AU044919.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC010327; AAH10327.1; -  
DR MGI: MGI:2144967; AU044919.  
DR InterPro: IPR003006; I9\_MHC.  
DR InterPro: IPR003006; I9\_MHC.  
DR Pfam: PF00047; I9; 3.  
DR PROSITE: PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.

KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 74.4%; Score 471; DB 11; Length 473;  
Best Local Similarity 75.4%; Pred. No. 8.8e-39;  
Matches 89; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVOLOESGGGLVKKPGSGSLKSCASGFTFSYVWVWQPEKRLLEVAVATISDGSSTYY 60  
DB 20 EVQLVESGGGLVKKPGSGSLKSCASGFTFSYVWVWQPEKRLLEVAVATISDGSSTYY 79  
QY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEPTAMYYCSR--RYDDAMDYWGCGTTVTVSS 118  
DB 80 ADVTKGRFTISRDNKNNLYLQMSLSKSEPTAMYYCARDMGSGPRGGISRPDIWGCGTTI 137

RESULT 4  
Q91207 PRELIMINARY; PRT; 486 AA.  
AC Q91207;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
DE Hypothetical 52.7 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC010324; AAH10324.1; -  
DR InterPro: IPR003598; I9\_C2.  
DR InterPro: IPR003006; I9\_MHC.  
DR Pfam: PF00047; I9; 4.  
DR SMART: SM00408; IGC2; 1.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein: Immunoglobulin domain.  
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 72.0%; Score 455.5; DB 11; Length 486;  
Best Local Similarity 72.6%; Pred. No. 3.2e-37;  
Matches 90; Conservative 10; Mismatches 17; Indels 7; Gaps 3;

QY 1 QVOLOESGGGLVKKPGSGSLKSCASGFTFSYVWVWQPEKRLLEVAVATISDGSSTYY 60  
DB 20 EVQLVESGGGLVKKPGSGSLKSCASGFTFSYVWVWQPEKRLLEVAVATISDGSSTYY 78  
QY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEPTAMYYCSR-----YRYPDAMDYWGCGTTV 114  
DB 79 PDNVKGRFTISRDNKNNLYLQMSLSKSEPTAMYYCARDMGSGPRGGISRPDIWGCGTTI 138

QY 115 TVSS 118  
DB 139 TVSS 142

RESULT 5  
Q91XEL PRELIMINARY; PRT; 480 AA.  
AC Q91XEL;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
DE Unknown (Protein for IMAGE:4224494) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-COLON;

RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC010798; AAH10798.1; -  
DR InterPro: IPR003006; IG\_MHC.  
DR Pfam: PF00047; Ig; 4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
FT NON\_TER  
KW  
SQ SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;  
  
Query Match  
Best Local Similarity 74.8%; Score 449.5; DB 11; Length 480;  
Matches 89; Conservative 11; Mismatches 14; Indels 5; Gaps 2;  
  
OY 2 VOLQESGGGLVPGGSLKLSCAASGFTFSDDYMWVWROTPEKRLKLEWVATISDGSYYTP 61  
DB 20 VKLVSSGGGLVPGGSLKLSCAASGFTFSNSMSVWROTPEKRLKLEWVATISNGVATHTP 79  
OY 62 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSR--YRYDAMDYWGCGTYYVSS 118  
DB 80 DSMKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSR--YRYDAMDYWGCGTYYVSS 135  
  
RESULT 6  
O91WP5 PRELIMINARY: PRT; 479 AA.  
AC O91WP5;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Hypothetical 51.6 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC013656; AAH13656.1; -  
DR InterPro: IPR003598; IG\_C2.  
DR InterPro: IPR003006; IG\_MHC.  
DR Pfam: PF00047; Ig; 4.  
DR SMART: SM00408; IGC2; 1.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein; Immunoglobulin domain.  
SQ SEQUENCE 479 AA; 51603 MW; ECB2D087748584F CRC64;  
  
Query Match  
Best Local Similarity 73.7%; Score 446.5; DB 11; Length 479;  
Matches 87; Conservative 9; Mismatches 19; Indels 3; Gaps 1;  
  
OY 1 OVQLOESGGGLVPGGSLKLSCAASGFTFSDDYMWVWROTPEKRLKLEWVATISDGSYYTP 60  
DB 20 EVQLVESGGGLVPGGSLKLSCAASGFTFSNYAMSVWROTPEKRLKLEWVAINSNGNTYY 79  
OY 61 PSDVKGRTISRDNKNNLYLQMSLSKSEDTAMYYCSR--YRYDAMDYWGCGTYYVSS 118  
DB 80 SDTMKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSR--YRYDAMDYWGCGTYYVSS 134  
  
RESULT 7  
O8TC77 PRELIMINARY: PRT; 471 AA.  
AC O8TC77;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Hypothetical 51.8 kDa protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SPLEEN;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC024289; AAH24289.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 471 AA; 51791 MW; 388F74CF58660E CRC64;  
  
Query Match  
Best Local Similarity 69.8%; Score 442; DB 4; Length 471;  
Matches 87; Conservative 12; Mismatches 16; Indels 10; Gaps 2;  
  
OY 1 OVQLOESGGGLVPGGSLKLSCAASGFTFSDDYMWVWROTPEKRLKLEWVATISDGSYYTP 60  
DB 20 EVQLVESGGGLVPGGSLKLSCAASGFTFSYAMSVWROTPEKRLKLEWVATISDGSYYTP 79  
OY 61 PSDVKGRTISRDNKNNLYLQMSLSKSEDTAMYYCSR-----YRYDAMDYWGCGT 113  
DB 80 ADSVKGRTISRDNKNNLYLQMSLSKSEDTAMYYCAR---FDVMGAGTYYVSS 136  
OY 114 VTSS 118  
DB 137 VTSS 141  
  
RESULT 8  
O9RI44 PRELIMINARY: PRT; 437 AA.  
AC O9RI44;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Gamma1 heavy chain of Mab7 (Fragment).  
GN IGH-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;  
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
RT antibody (Mab 7, its light and heavy chains) and construction of a  
RT single chain antibody (scFv)."  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF152372; AAD40243.1; -  
DR HSP: P01842; 7FAB.  
DR MGD: MG196446; Igh-4.  
DR InterPro: IPR003600; Ig\_Like.  
DR InterPro: IPR003006; IG\_Like.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; Ig; 4.  
DR SMART: SM00406; IGV; 1.  
DR SMART: SM00410; IGLike; 2.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
FT NON\_TER  
KW  
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;  
  
Query Match  
Best Local Similarity 75.2%; Score 433; DB 11; Length 437;  
Matches 88; Conservative 6; Mismatches 19; Indels 4; Gaps 2;  
  
OY 2 VOLQESGGGLVPGGSLKLSCAASGFTFSDDYMWVWROTPEKRLKLEWVATISDGSYYTP 61  
DB 1 VOLQESGGGLVPGGSLKLSCAASGFTFSYAMSVWROTPEKRLKLEWVATISDGSYYTP 59  
OY 62 DSVKGRFTISRDNKNNLYLQMSLSKSEDTAMYYCSR--YRYDAMDYWGCGTYYVSS 118  
DB 60 DSVKGRFTISKKNNILSLQMSLSKSEDTAMYYCAR---GDYSAVWGCGTYYVSS 113

RESULT 9  
09HCC1 PRELIMINARY; PRT; 112 AA.  
AC 09HCC1;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Single chain Fv (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;  
RT "An antibody fragment2A3 specific for native lysozyme: isolation from a  
human synthetic phage display library and characterization.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB049915; BAB16829.1; -  
DR HSSP; P01772; 2FB4.  
DR InterPro: IPR003599; Iq.  
DR InterPro: IPR003600; Iq\_Like.  
DR InterPro: IPR003006; Iq\_MHC.  
DR InterPro: IPR003596; Iq\_V.  
DR Pfam; PF00047; Iq; 1.  
DR SMART; SM00409; Iq; 1.  
DR SMART; SM00406; IqV; 1.  
DR SMART; SM00410; Iq\_Like; 1.  
FT NON\_TER 1 1  
FT SEQUENCE 112 AA; 12243 MW; 24F1A5EC3B84788 CRC64;  
Query Match 68.1%; Score 431; DB 4; Length 112;  
Best Local Similarity 71.9%; Pred. No. 1.5e-35;  
Matches 82; Conservative 14; Mismatches 16; Indels 2; Gaps 1;  
QY 1 QVLOESGGGLVPRGSGSLKSCAASGFTFSDYYWYWRQTPERKLEWVATISDGSYTY 60  
DB 1 EVOLVESGGGVPRGSGSLRISCAASGFTFPDQYMSVWRQAPGKGLWVSGINMGSGSTGY 60  
QY 61 PDSYKGRFTISRDNKAKNNLYLQMSLSKSEDTAMYYCSRYRYDDAMDYWGCTVTV 114  
DB 61 ADSYKGRFTISRDNKAKNNLYLQMSLSKSEDTAMYYCARRRY--ALDWYGCTTV 112  
RESULT 10  
09UL90 PRELIMINARY; PRT; 113 AA.  
AC 09UL90;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035024; AAD56260.1; -  
DR HSSP; P01772; 2FB4.  
DR InterPro: IPR003006; Iq\_MHC.  
DR InterPro: IPR003596; Iq\_V.  
DR Pfam; PF00047; Iq; 1.  
DR SMART; SM00406; IqV; 1.  
FT NON\_TER 1 1  
FT SEQUENCE 113 AA; 12433 MW; 24F1A5EC3B84788 CRC64;

FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;  
Query Match 68.0%; Score 430.5; DB 4; Length 113;  
Best Local Similarity 70.3%; Pred. No. 1.7e-35;  
Matches 83; Conservative 14; Mismatches 16; Indels 5; Gaps 1;  
QY 1 QVLOESGGGLVPRGSGSLKSCAASGFTFSDYYWYWRQTPERKLEWVATISDGSYTY 60  
DB 1 EVOLVESGGGVPRGSGSLRISCAASGFTFSSGMHWWRQAPGKGLWVATIRYDSMKY 60  
QY 61 PDSYKGRFTISRDNKAKNNLYLQMSLSKSEDTAMYYCSRYRYDDAMDYWGCTVTV 118  
DB 61 ADSYKGRFTISRDNKAKNNLYLQMSLSKSEDTAMYYCARRRY-----DLNWDGCTTVTV 113  
RESULT 11  
09UL91 PRELIMINARY; PRT; 118 AA.  
AC 09UL91;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035023; AAD56259.1; -  
DR HSSP; P01772; 2FB4.  
DR InterPro: IPR003006; Iq\_MHC.  
DR InterPro: IPR003596; Iq\_V.  
DR Pfam; PF00047; Iq; 1.  
DR SMART; SM00406; IqV; 1.  
FT NON\_TER 1 1  
FT NON\_TER 118 118  
FT SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;  
Query Match 67.9%; Score 430; DB 4; Length 118;  
Best Local Similarity 71.8%; Pred. No. 2e-35;  
Matches 84; Conservative 11; Mismatches 22; Indels 0; Gaps 0;  
QY 1 QVLOESGGGLVPRGSGSLKSCAASGFTFSDYYWYWRQTPERKLEWVATISDGSYTY 60  
DB 1 EVOLVESGGGVPRGSGSLRISCAASGFTFSSYNNWRQAPGKGLWVATISSTITITTY 60  
QY 61 PDSYKGRFTISRDNKAKNNLYLQMSLSKSEDTAMYYCSRYRYDDAMDYWGCTVTV 117  
DB 61 ADSYKGRFTISRDNKAKNNLYLQMSLSKSEDTAMYYCARRDSSEAFDWMGCTVTV 117  
RESULT 12  
09UL71 PRELIMINARY; PRT; 121 AA.  
AC 09UL71;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;

[1]  
SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL: AF035043; AAD56279.1; -  
DR HSSP: P01772; 12EB4.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; 1g.1.  
DR SMART: SM00406; IGv.1.  
FT NON\_TER 1  
FT 121 121  
SO SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 67.9%; Score 429.5; DB 4; Length 121;  
Best Local Similarity 67.8%; Pred. No. 2.3e-35;  
Matches 82; Conservative 15; Mismatches 21; Indels 3; Gaps 1;

OY 1 OVOLOESGGGLVPGSGSLKSCASGFTFSDYYWVWVROTPKRLKLEWVATISDGSSTYY 60  
DB 1 EVQLVESGGGVYVPGSGSLRLECAASGFTFDGYAMHWVROAPGKLEWVSLISDGSSTYY 60  
OY 61 PDSVAGRTTISDNKNNLYLQMSLSKSEDTAMVYCSRRYD---DAMDYMGCGTTVTVS 117  
DB 61 ADSVAGRTTISDNKNSLYLQMSLRAEDTALVYCAKGGKVTIYDRDIDMGCGTMYVS 120  
OY 118 S 118  
DB 121 S 121

RESULT 13  
O8WUK1 PRELIMINARY: PRT: 613 AA.  
ID O8WUK1;  
AC O8WUK1;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Hypothetical 67.3 kDa protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN 111  
RP SEQUENCE FROM N.A.  
RC TISSUE=TONSIL;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC020240; AAH20240.1; -  
DR InterPro: IPR003599; 1g.  
DR InterPro: IPR003597; IG\_C1.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; 1g.5.  
DR SMART: SM00409; IG; 2.  
DR SMART: SM00407; IG\_C1; 4.  
DR SMART: SM00406; IGv.1.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_3.  
KW Hypothetical protein.  
SO SEQUENCE 613 AA; 67296 MW; 60C7F950671E315 CRC64;

Query Match 67.5%; Score 427; DB 4; Length 613;  
Best Local Similarity 70.0%; Pred. No. 3e-34;  
Matches 84; Conservative 13; Mismatches 21; Indels 2; Gaps 1;

OY 1 OVOLOESGGGLVPGSGSLKSCASGFTFSDYYWVWVROTPKRLKLEWVATISDGSSTYY 60  
DB 20 OVOLOESGGGVYVPGSGSLRLECAASGFTFSDGYAMHWVROAPGKLEWVAVISDGSSTYY 79

OY 61 PDSVAGRTTISDNKNNLYLQMSLSKSEDTAMVYCSRRYD---DAMDYMGCGTTVTVS 118  
DB 80 ADSVAGRTTISDNKNSLYLQMSLRAEDTALVYCAKGGKVTIYDRDIDMGCGTMYVS 139

RESULT 14  
O96K68 PRELIMINARY: PRT: 494 AA.  
ID O96K68;  
AC O96K68;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE CDNA FLJ14473 fis, clone MAMMA1001080, highly similar to Homo  
DE sapiens SNC73 protein (SNC73) mRNA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN 111  
RP SEQUENCE FROM N.A.  
RC TISSUE=MAMMARY GLAND;  
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
RA Wagaatsuma M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,  
RA Niinomiya K., Iwayanagi T.;  
RT "NEBO human cDNA sequencing project.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AK027379; BAB55072.1; -  
DR InterPro: IPR003006; IG\_MHC.  
DR Pfam: PF00047; 1g.4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
SO SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AE4C0E CRC64;

Query Match 67.1%; Score 425; DB 4; Length 494;  
Best Local Similarity 66.9%; Pred. No. 3.6e-34;  
Matches 84; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

OY 1 OVOLOESGGGLVPGSGSLKSCASGFTFSDYYWVWVROTPKRLKLEWVATISDGSSTYY 60  
DB 20 EVQLVESGGGLVPGSGSLRLECAASGSLSPSTYAMMWVROAPGKLEWVSSISSRSDIY 79  
OY 61 PDSVAGRTTISDNKNNLYLQMSLSKSEDTAMVYCSRRYDANDY---WGCGTTVTV 116  
DB 80 PDSVAGRTTISDNKNSLYLQMSLRAEDTALVYCAKGGKVTIYDRDIDMGCGTMYVS 139  
OY 117 S 118  
DB 140 SS 141

RESULT 15  
O96BB9 PRELIMINARY: PRT: 597 AA.  
ID O96BB9;  
AC O96BB9;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Hypothetical 65.0 kDa protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN 111  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-CELL;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC015760; AAH15760.1; -  
DR InterPro: IPR003006; IG\_MHC.  
DR Pfam: PF00047; 1g.5.

DR	PROSITE; PS00290; IG_MHC	UNKNOWN_3.
KW	Hypothetical protein.	
SO	SEQUENCE 597 AA; 65039 MW; 4FGCA3AD8ECE263D9 CRC64;	



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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:10:24 : Search time 13.6348 Seconds  
(without alignments)  
789.676 Million cell updates/sec

Title: US-09-144-886-87

Perfect score: 586

Sequence: 1 DIETQSPASLAVSLGGRAT.....QQSNDEPFTGSGTKLEIKR 112

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	539	92.0	111	1 KYMS37	Ig kappa chain V r
2	519	88.6	107	2 S26343	Ig kappa chain V r
3	515	87.9	115	2 S63596	Ig kappa chain V r
4	512	87.4	107	2 S26344	Ig kappa chain V r
5	512	87.4	131	1 KYMSM6	Ig kappa chain pre
6	508	86.7	132	1 KYMS32	Ig kappa chain pre
7	500	85.3	111	2 S09965	Ig kappa chain V-J
8	498	85.0	111	1 KYMS43	Ig kappa chain V r
9	496	84.6	111	2 D45722	Ig kappa chain V r
10	493	84.1	111	2 KYMS08	Ig kappa chain V r
11	487	83.1	111	1 KYMS83	Ig kappa chain V r
12	486	82.9	111	1 KYMS69	Ig kappa chain V r
13	482	82.3	111	2 E53285	Ig kappa chain V a
14	480	81.9	111	1 KYMSCL	Ig kappa chain V r
15	477	81.4	112	2 S19972	Ig kappa chain V r
16	473	80.7	112	2 S19971	Ig kappa chain V r
17	471	80.4	112	2 S19976	Ig kappa chain V r
18	468.5	79.9	110	1 KYMS10	Ig kappa chain V r
19	468	79.9	131	2 PH1226	Ig kappa chain pre
20	467	79.7	111	1 KYMS75	Ig kappa chain V r
21	465	79.4	111	1 KYMS40	Ig kappa chain V r
22	465	79.4	111	1 KYMS40	Ig kappa chain V r
23	463	79.0	111	1 KYMS80	Ig kappa chain V r
24	462	78.8	210	2 A56169	Ig kappa chain V r
25	458	78.2	111	2 A33936	Ig kappa chain V r
26	457	78.0	111	2 S09965	Ig kappa chain V r
27	456	77.8	111	2 PH0081	Ig kappa chain V-J
28	456	77.8	112	2 S45715	Ig kappa chain V r
29	456	77.8	218	2 JC5810	monoclonal antibody

30	455	77.6	111	1 KYMS50	Ig kappa chain V r
31	455	77.6	111	1 KYMS85	Ig kappa chain V r
32	452	77.1	218	2 S68241	Ig kappa chain V r
33	449	76.6	111	2 S09966	Ig kappa chain V-J
34	447	76.3	111	2 S09963	Ig kappa chain V-J
35	447	76.3	131	2 S55027	Ig light chain pre
36	435.5	74.3	110	2 S24288	Ig kappa chain V r
37	434	74.1	109	2 PH0093	Ig kappa chain V r
38	434	74.1	111	2 S37202	Ig kappa chain V r
39	432	73.7	96	2 B49442	Ig kappa chain V r
40	427	72.9	108	1 KYMS54	Ig kappa chain V r
41	426	72.7	111	1 KYMS13	Ig kappa chain V r
42	426	72.7	140	2 PN0446	Ig kappa chain pre
43	420	71.7	120	2 S06731	Ig kappa chain pre
44	418	71.3	102	2 PH1079	Ig light chain V r
45	416.5	71.1	108	2 PH0092	Ig kappa chain V r

#### ALIGNMENTS

```
RESULT 1
KYMS37
Ig kappa chain V regions (PC3741, T111) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 21-Jan-2000
C:Accession: A93204; A93822; A01934
R:Weigert, M.; Galimuljan, L.; Ioh, E.; Schilling, J.; Hood, L.
N:ature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152; PMID:103003
A:Contents: PC3741
A:Accession: A93204
A:Molecule type: protein
A:Residues: 1-111 <WEI>
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related
A:Reference number: A93822; MUID:79012520; PMID:99744
A:Contents: T111
A:Accession: A93822
A:Molecule type: protein
A:Residues: 1-111 <MCK>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match          92.0%; Score 539; DB 1; Length 111;
Best Local Similarity 93.7%; Pred. No. 6.8e-41;
Matches 104; Conservative
2; Mismatches 5; Indels 0; Gaps 0;

OY 1 DIETQSPASLAVSLGGRATISCRASEYSDYSGHSPMVOOKPGQPKLLYRASNLPP 60
DB 1 DVLVQSPASLAVSLGGRATISCRASEYSDYSGHSPMVOOKPGQPKLLYRASNLBS 60
OY 61 GIPARESGSGRTDFTLTINPVADVDVATYYCOQSNDEPFTGSGTKLEIKR 111
DB 61 GIPARESGSGRTDFTLTINPVADVDVATYYCOQSNDEPFTGSGTKLEIKR 111

RESULT 2
S26343
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26343
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421; PMID:1908510
```



F:21-131/Domain: Ig kappa chain precursor V region #status experimental <MAT>  
F:36-114/Domain: Immunoglobulin homology <IMM>  
F:43-112/Disulfide bonds: #status predicted

Query Match 87.4% Score 512; DB 1; Length 131;  
Best Local Similarity 88.3% Pred. No. 1.9e-38;  
Matches 98; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGQRTATSCRASESVDYSGHFMQWYQKPGQPPKLLIYRASNLDP 60  
D 21 NIVLTQSPASLAVSLGQRTATSCRASESVDYSGHFMQWYQKPGQPPKLLIYRASNLDS 80

QY 61 GIPARFSGSGSGTDFTLTINPEADVAITYCOQSNEDPFFGSGTKLEIK 111  
D 81 GIPARFSGSGSGRTDFTLTIDPEADDAITYCCQNNEDPWFPGSGTKLEIK 131

## RESULT 6

KVMS32

Ig kappa chain precursor V regions (MOPC 321, TEPC 124) - mouse (tentative sequence)

C:Species: Mus musculus (house mouse)

C:Date: 31-May-1979 #sequence\_revision 31-May-1979 #text\_change 31-Mar-2000

C:Accession: A90412; A90373; A90374; A01933

R:Birstein, Y.; Schechter, I.

R:Biochemistry 17, 2392-2400, 1978

A:Title: Primary structures of N-terminal extra peptide segments linked to the variable expression of immunoglobulin genes.

A:Reference number: A90412; MUID:78235887; PMID:98179

A:Contents: MOPC 321

A:Accession: A90412

A:Molecule type: protein

A:Residues: 1-37 <BUR>

R:McKean, D.; Potter, M.; Hood, L.

R:Biochemistry 12, 749-759, 1973

A:Title: Mouse immunoglobulin chains. Partial amino acid sequence of a kappa chain.

A:Reference number: A90373; MUID:73140224; PMID:4120629

A:Contents: MOPC 321

A:Accession: A90373

A:Molecule type: protein

A:Residues: 21-132 <MCK>

A:Note: The partial sequence of the C region of this Bence Jones protein was also determined.

R:McKean, D.; Potter, M.; Hood, L.

R:Biochemistry 12, 760-771, 1973

A:Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains

A:Reference number: A90374; MUID:73140225; PMID:4651517

A:Contents: TEPC 124

A:Accession: A90374

A:Molecule type: protein

A:Residues: 21-131 <MC2>

A:Note: The sequence is compatible with that of MOPC 321 except in having 47-Glx, 51-Trp

C:Comment: The MOPC 321 sequence is shown.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1d

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-132/Product: Ig kappa chain V regions (MOPC 321, TEPC 124) #status predicted <MAT>

F:36-114/Domain: immunoglobulin homology <IMM>

F:43-112/Disulfide bonds: #status predicted

Query Match 86.7% Score 508; DB 1; Length 132;  
Best Local Similarity 79.5% Pred. No. 4.4e-38;  
Matches 99; Conservative 20; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGQRTATSCRASESVDYSGHFMQWYQKPGQPPKLLIYRASNLDP 60  
D 21 NIVLTQSPASLAVSLGQRTATSCRASESVDYSGHFMQWYQKPGQPPKLLIYRASNLDS 80

QY 61 GIPARFSGSGSGTDFTLTINPEADVAITYCOQSNEDPFFGSGTKLEIK 112  
D 81 GIPARFSGSGSGRTDFTLTIDPEADDAITYCCQNNEDPWFPGSGTKLEIK 132

## RESULT 7

S09965

Ig kappa chain V-J region (106-10E) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 21-Jan-2000

C:Accession: S09965

R:Reininger, L.; Shiba, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.

R:Eur. J. Immunol. 20, 771-777, 1990

A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibody

A:Reference number: S09965; MUID:90269328; PMID:2347362

A:Accession: S09965

A:Molecule type: mRNA

A:Residues: 1-111 <RET>

A:Cross-references: EMBL:Z51853; NID:955394; PIDN:CA83146.1; PID:9930230

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 85.3% Score 500; DB 2; Length 111;  
Best Local Similarity 87.4% Pred. No. 1.9e-37;  
Matches 97; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGQRTATSCRASESVDYSGHFMQWYQKPGQPPKLLIYRASNLDP 60  
D 21 NIVLTQSPASLAVSLGQRTATSCRASESVDYSGHFMQWYQKPGQPPKLLIYRASNLDS 80  
QY 61 GIPARFSGSGSGTDFTLTINPEADVAITYCOQSNEDPFFGSGTKLEIK 111  
D 81 GIPARFSGSGSGRTDFTLTIDPEADDAITYCCQNNEDPWFPGSGTKLEIK 131

## RESULT 8

KVMS43

Ig kappa chain V region (PC7043) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000

C:Accession: A01937; S42187; S42190; S42188; S42191; S42192

R:Weigert, M.; Garbalian, L.; Loh, E.; Schilling, J.; Hood, L.

R:Nature 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: A01937

A:Molecule type: protein

A:Residues: 1-111 <WEI>

R:Mo, J.A.; Bona, C.A.; Holmdahl, R.

R:Eur. J. Immunol. 23, 2503-2510, 1993

A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42187

A:Molecule type: DNA

A:Residues: 12-99 <MO>

A:Cross-references: EMBL:Z25458; NID:9407844; PIDN:CA80945.1; PID:9407845

A:Note: V-kappa-21E; anti-collagen

A:Accession: S42190

A:Molecule type: DNA

A:Residues: 13-99 <MO>

A:Cross-references: EMBL:Z25450; NID:9407838; PIDN:CA80937.1; PID:9407839

A:Note: V-kappa-21E; anti-collagen

A:Accession: S42189

A:Molecule type: DNA

A:Residues: 15-99 <MO>

A:Cross-references: EMBL:Z25448; NID:9407836; PIDN:CA80935.1; PID:9407837

A:Note: V-kappa-21E; anti-collagen

A:Accession: S42188

A:Molecule type: DNA

A:Residues: 12-99 <MO>

A:Cross-references: EMBL:Z25446; NID:9407834; PIDN:CA80933.1; PID:9407835



Best Local Similarity 82.9%; Pred. No. 1.1e-35;

Search completed: January 13, 2003, 15:13:12  
Job time : 13.6348 secs

Job time : 13.6348 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2003, 15:08:33 : Search time 8.72174 Seconds  
(without alignments)  
561.150 Million cell updates/sec

Title: US-09-144-886-63

Perfect score: 633

Sequence: 1 OVOLOESGGGLVKGSLK.....YRYDANDYWGCGTIVYSS 118

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	508	80.3	98	1 HV57_MOUSE	P18528 mus musculus
2	452	71.4	136	1 HV16_MOUSE	P01783 mus musculus
3	448	70.8	117	1 HV54_MOUSE	P18525 mus musculus
4	443	70.0	117	1 HV55_MOUSE	P18526 mus musculus
5	439	69.4	117	1 HV58_MOUSE	P18529 mus musculus
6	437.5	69.1	97	1 HV56_MOUSE	P18527 mus musculus
7	431	68.1	117	1 HV59_MOUSE	P18530 mus musculus
8	425	67.1	122	1 HV3G_HUMAN	P01768 homo sapien
9	419	66.2	117	1 HV53_MOUSE	P01762 homo sapien
10	413	65.2	122	1 HV3A_HUMAN	P01771 homo sapien
11	404.5	63.9	121	1 HV3J_HUMAN	P01772 homo sapien
12	403	63.7	126	1 HV3K_HUMAN	P01770 homo sapien
13	401	63.3	111	1 HV35_MOUSE	P01804 mus musculus
14	398	62.9	119	1 HV38_MOUSE	P01784 mus musculus
15	397	62.7	114	1 HV3B_HUMAN	P01763 homo sapien
16	396	62.6	119	1 HV37_MOUSE	P01807 mus musculus
17	395	62.6	119	1 HV4Q_MOUSE	P01810 mus musculus
18	395	62.4	116	1 HV3T_HUMAN	P01781 homo sapien
19	393.5	62.2	119	1 HV3I_HUMAN	P01780 homo sapien
20	392.5	62.0	113	1 HV30_MOUSE	P01799 mus musculus
21	392.5	62.0	113	1 HV32_MOUSE	P01801 mus musculus
22	390.5	61.7	118	1 HV39_MOUSE	P01809 mus musculus
23	390	61.6	117	1 HV3C_HUMAN	P01764 homo sapien
24	388	61.3	122	1 HV2Q_MOUSE	P01789 mus musculus
25	387.5	61.2	119	1 HV3L_HUMAN	P01767 homo sapien
26	386.5	61.1	115	1 HV3F_HUMAN	P01773 homo sapien
27	385.5	60.9	113	1 HV2I_MOUSE	P01788 mus musculus
28	385.5	60.9	123	1 HV19_MOUSE	P01790 mus musculus
29	385	60.8	122	1 HV21_MOUSE	P01802 mus musculus
30	384.5	60.7	115	1 HV33_MOUSE	P01784 canis fam11
31	384	60.7	114	1 HV01_CANFA	P01811 mus musculus
32	383.5	60.6	117	1 HV41_MOUSE	P01791 mus musculus
33	383.5	60.6	123	1 HV22_MOUSE	

34	382.5	60.4	113	1 HV31_MOUSE	P01800 mus musculus
35	382.5	60.4	123	1 HV25_MOUSE	P01794 mus musculus
36	381.5	60.3	116	1 HV05_CARAU	P19181 carassius a
37	381.5	60.3	123	1 HV18_MOUSE	P01787 mus musculus
38	381.5	60.3	123	1 HV23_MOUSE	P01792 mus musculus
39	381.5	60.3	123	1 HV24_MOUSE	P01793 mus musculus
40	381	60.2	112	1 HV3H_HUMAN	P01769 homo sapien
41	379.5	60.0	113	1 HV28_HUMAN	P01797 mus musculus
42	378.5	59.8	117	1 HV02_CANFA	P01785 canis fam11
43	378.5	59.8	144	1 HV26_MOUSE	P01795 mus musculus
44	376.5	59.5	142	1 HV01_RAT	P01805 ratius norv
45	375.5	59.3	113	1 HV29_MOUSE	P01798 mus musculus

## ALIGNMENTS

```

RESULT 1
HV57_MOUSE
ID HV57_MOUSE
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DR 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 6.96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCB1_Taxid=10090;
RN [1]
RC STRAIN-BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpietro U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -! MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J10501; HVMS96.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; ISG_1.
KW Immunoglobulin V region.
FT NON_TER
SQ SEQUENCE 98 AA; 11007 MW; B8644F7E92F8F95B CRC64;

Query Match
Best local Similarity 96.9%; Pred. No. 4.7e-45;
Matches 95; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OVOLOESGGGLVKGSLKSCAASGFTFSDDYMYVWRQTPPEKRLBMTATISDGSYTY 60
Db 1 EVGLVSGGGLVKGSLKSCAASGFTFSDDYMYVWRQTPPEKRLBMTATISDGSYTY 60
QY 61 PDSVKGRTISRDNKNNLYLQMSLSKSEDTATYCSR 98
Db 61 PDSVKGRTISRDNKNNLYLQMSLSKSEDTATYCAR 98

RESULT 2
HV16_MOUSE
ID HV16_MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_Taxid=10090;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Rothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adeugbo K., Mlstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC -----
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CC -----
CC EMBL: J00522; AAD15290.1; -.
DR PIR: A02066; G1MS21.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR Immunoglobulin V region; Signal.
KW NON_TER 1
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90 DN -> DYAH (IN REF. 2).
FT CONFLICT 115 115 DN -> ND (IN REF. 2).
FT CONFLICT 120 120 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON_TER 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;

Query Match
Best Local Similarity 75.0%; Score 452; DB 1; Length 136;
Matches 90; Conservative 10; Mismatches 16; Indels 4; Gaps 2;

QY 2 VQLOESGGGLVPGGSLKSCAASGFTFSDYYMYWVROTPERKLEWVAITSDGGSTYY 61
Db 18 VQLVESGGGLVPGGSKRLSCAASGFTFSSFGMHVROAPEKLEWVAITSSGSTLHYA 77
QY 62 DSVYGRFTISRDNKNNLYLQMSLSKSEDPAMYCSR---YRYDADNDYMGCTTVYSS 118
Db 78 DTVYGRFTISRDNKNNLYLQMTSLRSEDPAMYCARWGNPY-YAMDYMGCTSVYSS 136

RESULT 3
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;

```

```

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: JTO505; HVMS84.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR Immunoglobulin V region; Signal.
KW NON_TER 1
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARTY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARTY-DETERMINING-2.
FT DISULFID 86 117 FRAMEWORK-3.
FT NON_TER 41 115 BY SIMILARITY.
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match
Best Local Similarity 70.8%; Score 448; DB 1; Length 117;
Matches 85; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVLOESGGGLVPGGSLKSCAASGFTFSDYYMYWVROTPERKLEWVAITSDGGSTYY 60
Db 20 EVKLVESGGGLVPGGSLKSCAASGFTFSSYMYWVROTPERKLEWVAITSDGGSTYY 79
QY 61 PDSYGRFTISRDNKNNLYLQMSLSKSEDPAMYCSR 98
Db 80 PDSYGRFTISRDNKNNLYLQMSLSKSEDPAMYCAR 117

RESULT 4
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: JTO502; HVMS34.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR Immunoglobulin V region; Signal.
KW NON_TER 1
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARTY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARTY-DETERMINING-2.
FT DISULFID 86 117 FRAMEWORK-3.
FT NON_TER 41 115 BY SIMILARITY.

```



FT	DOMAIN	55	68	FRAMEWORK-2.
FT	DOMAIN	69	85	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	86	117	FRAMEWORK-3.

1 QVQLQESGGGLV<sup>1</sup>PGGSLK<sup>1</sup>LSCAASGFT<sup>1</sup>FDY<sup>1</sup>MYWV<sup>1</sup>RQTP<sup>1</sup>PEKRL<sup>1</sup>EWAT<sup>1</sup>ISDGGST<sup>1</sup>YY<sup>1</sup> 60

FT	DOMAIN	20	43	FRAMEWORK-1.
FT	DOMAIN	50	54	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	55	68	FRAMEWORK-2.
FT	DOMAIN	69	85	COMPLEMENTARITY-DETERMINING-2.



KW Immunoglobulin V region.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA: 13472 MW: 2821A11DA04D80F9 CRC64:  
Query Match 65.2%; Score 413; DB 1; Length 122;  
Best Local Similarity 60.7%; Pred. No. 2,8e-35;  
Matches 74; Conservative 22; Mismatches 22; Indels 4; Gaps 1;  
OY 1 OVQLOESGGGLVPGSGSLKSCAASGFTFSDYYMWVROTPEKRLKLEWVATISDGSYYTY 60  
DB 1 OVQLOVSGGGGLVPGSGSLKSCAASGFTFSDYYMWVROTPEKRLKLEWVATISDGSYYTY 60  
OY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYD-----AMDYWGQCTTVY 116  
DB 61 ADSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYD-----AMDYWGQCTTVY 120  
OY 117 SS 118  
DB 121 SS 122  
RESULT 11  
HV3K\_HUMAN STANDARD: PRT; 126 AA.  
ID HV3K\_HUMAN  
AC P01772:  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-II region H1L.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=79124695; PubMed=420800;  
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;  
RT "Amino acid sequence of the VH region of human myeloma  
cytoimmunoglobulin IgG H1L";  
RL Biochemistry 18:553-560(1979).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGGI MYELOMA  
CC PROTEIN.  
DR PIR: A02054; G1HUKL.  
DR HSSP: P01772; 2PB4.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; Ig\_V.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT NON\_TER 121 121  
SQ SEQUENCE 121 AA: 13566 MW: 480FC53610EF5DAB CRC64:  
Query Match 63.9%; Score 404.5; DB 1; Length 121;  
Best Local Similarity 63.7%; Pred. No. 2e-34;  
Matches 79; Conservative 17; Mismatches 19; Indels 9; Gaps 2;  
OY 1 OVQLOESGGGLVPGSGSLKSCAASGFTFSDYYMWVROTPEKRLKLEWVATISDGSYYTY 60  
DB 1 OVQLOVSGGGGLVPGSGSLKSCAASGFTFSDYYMWVROTPEKRLKLEWVATISDGSYYTY 60  
OY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYD-----AMDYWGQCTTVY 114  
DB 61 GDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYD-----AMDYWGQCTTVY 117  
OY 115 TVSS 118  
DB 118 TVSS 121;  
RESULT 12  
HV3K\_HUMAN

ID HV3K\_HUMAN STANDARD: PRT; 126 AA.  
AC P01772:  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-II region KOL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=83289131; PubMed=688494;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary  
structure of crystallized monoclonal immunoglobulin IgG1 KOL, I";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
RA MEDLINE=81072295; PubMed=7441755;  
RA Marguaret M., Deisenhofer J., Huber R., Palm W.;  
RT "Crystallographic refinement and atomic models of the intact  
immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A  
and 1.0-A resolution.";  
RL J. Mol. Biol. 141:369-391(1980).  
DR PIR: A02055; G1HUKL.  
DR PDB: 2PB4; 12-JUL-89.  
DR PDB: 2IG2; 12-JUL-89.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; Ig\_V; 1.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region; 3D-structure.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 96  
FT DISULFID 105 110  
FT STRAND 3 7  
FT STRAND 11 12  
FT STRAND 14 15  
FT STRAND 18 25  
FT STRAND 29 31  
FT STRAND 34 39  
FT STRAND 41 42  
FT STRAND 46 51  
FT TURN 53 54  
FT TURN 58 60  
FT TURN 62 67  
FT STRAND 68 73  
FT TURN 74 77  
FT STRAND 78 83  
FT STRAND 88 90  
FT HELIX 92 99  
FT STRAND 106 106  
FT TURN 107 108  
FT STRAND 109 109  
FT STRAND 113 113  
FT STRAND 120 124  
FT NON\_TER 126 126  
SQ SEQUENCE 126 AA: 13718 MW: EAD71B52B16F8776 CRC64:  
Query Match 63.7%; Score 403; DB 1; Length 126;  
Best Local Similarity 62.8%; Pred. No. 3e-34;  
Matches 81; Conservative 12; Mismatches 22; Indels 14; Gaps 2;  
OY 1 OVQLOESGGGLVPGSGSLKSCAASGFTFSDYYMWVROTPEKRLKLEWVATISDGSYYTY 60  
DB 1 OVQLOVSGGGGLVPGSGSLKSCAASGFTFSDYYMWVROTPEKRLKLEWVATISDGSYYTY 60  
OY 61 PDSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYD-----AMDYWG 109  
DB 61 ADSVKGRTTISRDNKNNLYLQMSLSKSEDTAMYYCSRRYD-----DGHGFCSSASCFFPDYWG 117  
OY 110 QCTTVTSS 118



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 15:08:33 : Search time 8.27826 Seconds  
(without alignments)  
561.150 Million cell updates/sec

Title: US-09-144-886-87

Perfect score: 586

Sequence: 1 DIETLOSPASLAVSLGQRAT.....QSNDEPFTFGSGTKLEIKR 112

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum db seq length: 0  
Maximum db seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	539	92.0	111	1 KV3H_MOUSE	P01660 mus musculus
2	514	87.7	111	1 KV3J_MOUSE	P01662 mus musculus
3	512	87.4	131	1 KV3I_MOUSE	P01661 mus musculus
4	510	87.0	111	1 KV3K_MOUSE	P01663 mus musculus
5	508	86.7	132	1 KV3F_MOUSE	P01658 mus musculus
6	501	85.5	112	1 KV3G_MOUSE	P01659 mus musculus
7	498	85.0	111	1 KV3M_MOUSE	P01665 mus musculus
8	493	84.1	111	1 KV3O_MOUSE	P01666 mus musculus
9	487	83.1	111	1 KV3N_MOUSE	P01667 mus musculus
10	486	82.9	111	1 KV3Q_MOUSE	P01669 mus musculus
11	480	81.9	111	1 KV3L_MOUSE	P01664 mus musculus
12	468.5	79.9	110	1 KV3P_MOUSE	P01668 mus musculus
13	467	79.4	111	1 KV3S_MOUSE	P01671 mus musculus
14	465	79.4	111	1 KV3R_MOUSE	P01670 mus musculus
15	465	79.4	111	1 KV3T_MOUSE	P01672 mus musculus
16	463	79.0	111	1 KV3A_MOUSE	P01654 mus musculus
17	456.5	77.9	112	1 KV3B_MOUSE	P01655 mus musculus
18	455	77.6	111	1 KV3D_MOUSE	P01657 mus musculus
19	453	77.6	111	1 KV3U_MOUSE	P01677 mus musculus
20	454	77.5	111	1 KV3C_MOUSE	P01656 mus musculus
21	427	72.9	108	1 KV3V_MOUSE	P01674 mus musculus
22	426	72.7	111	1 KV3E_MOUSE	P01657 mus musculus
23	400	68.3	114	1 KV4A_HUMAN	P01625 homo sapien
24	399	68.1	108	1 KV5P_MOUSE	P01649 mus musculus
25	394	67.2	134	1 KV4C_HUMAN	P06314 homo sapien
26	387.5	66.1	133	1 KV4B_HUMAN	P06313 homo sapien
27	380	64.8	108	1 KV1M_HUMAN	P01605 homo sapien
28	376	64.2	108	1 KV1L_HUMAN	P01604 homo sapien
29	373.5	63.7	129	1 KV3M_HUMAN	P18136 homo sapien
30	373	63.7	108	1 KV1H_HUMAN	P01600 homo sapien
31	373	63.7	108	1 KV1N_HUMAN	P01606 homo sapien
32	371.5	63.4	129	1 KV1L_HUMAN	P18135 homo sapien
33	371	63.3	108	1 KV1Y_HUMAN	P80362 homo sapien

34	371	63.3	129	1 KV1W_HUMAN	P04431 homo sapien
35	370.5	63.2	109	1 KV3D_HUMAN	P01622 homo sapien
36	370	63.1	108	1 KV1E_HUMAN	P01594 homo sapien
37	370	63.1	108	1 KV1E_HUMAN	P01597 homo sapien
38	370	63.1	108	1 KV1F_HUMAN	P01607 homo sapien
39	370	63.1	108	1 KV1O_HUMAN	P01620 homo sapien
40	369.5	63.1	109	1 KV3B_HUMAN	P04207 homo sapien
41	368.5	62.9	129	1 KV3H_HUMAN	P01608 homo sapien
42	368	62.8	108	1 KV1P_HUMAN	P04430 homo sapien
43	368	62.8	108	1 KV1V_HUMAN	P01596 homo sapien
44	366.5	62.5	107	1 KV1D_HUMAN	P01603 homo sapien
45	365	62.3	108	1 KV1K_HUMAN	

## ALIGNMENTS

RESULT 1					
ID	Sequence	Standard	PRT	111 AA	
KV3H_MOUSE					
AC	P01660:				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-II region PC 3741/TEPC 111.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE (PC 3741).				
RX	MEDLINE=79073152; PubMed=103003;				
RA	Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;				
RT	"Rearrangement of genetic information may produce immunoglobulin				
RT	diversity."				
RL	Nature 276:785-790(1978).				
RN	[2]				
RP	SEQUENCE (TEPC 111).				
RX	MEDLINE=79012520; PubMed=99744;				
RA	McKean D.J., Bell M., Potter M.;				
RT	"Mechanisms of antibody diversity: multiple genes encode structurally				
RT	related mouse kappa variable regions."				
RL	Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).				
CC	-I- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.				
DR	PIR: A01934; KVM37.				
DR	HSSP: P01679; 2F8U.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	Pfam: PF00047; Ig_1.				
DR	SMART: SM00406; IGV_1.				
KW	Immunoglobulin V region.				
FT	DOMAIN 1..23				FRAMEWORK-1.
FT	DOMAIN 24..38				COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 39..53				FRAMEWORK-2.
FT	DOMAIN 54..60				COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 61..92				FRAMEWORK-3.
FT	DOMAIN 93..101				COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN 102..111				FRAMEWORK-4.
FT	DISULFID 23..92				BY SIMILARITY.
FT	NON_TER 111..111				
SO	SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;				
Query Match					
Best Local Similarity 92.0%; Score 539; DB 1; Length 111;					
Matches 104; Conservative 2; Mismatches 5; Indels 0; Gaps 0;					
OY	1 DIETLOSPASLAVSLGQRATISCRASESDVSQSFPMOYQKPGQPKLLIYRASNLSP 60				
DB	1 DIETLOSPASLAVSLGQRATISCRASESDVSQSFPMOYQKPGQPKLLIYRASNLSP 60				
OY	61 GIPARFSGSGSGTDFLTITNPVADVDVATYYCCQSNDEPFTFGSGTKLEIK 111				
DB	61 GIPARFSGSGSGRTDFLTITNPVADVDVATYYCCQSNDEPFTFGSGTKLEIK 111				

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RESULT 2
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15 kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gaumatan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity."
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR HSP; P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IGV; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 87.7%; Score 514; DB 1; Length 111;
Best Local Similarity 88.3%; Pred. No. 1.le-46;
Matches 98; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIETGSPASLAVSLGGRATISCRASESVDSYGHSEFMQYQKRGOPPKLLIYRASLLEP 60
DB 1 NIYLTGSPASLAVSLGGRATISCRASESVDSYGHSEFMQYQKRGOPPKLLIYRASLLEP 60
QY 61 GIPARFSGSGGTFTLTINPEADVAITYCCQSNEDPFTFGSGTKLEIK 111
DB 61 GVPARFSGSGSRITDFTLTIDPVEADDAITYCCQNNEDPFTFGSGTKLEIK 111

RESULT 3
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15 kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burslein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes."
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences."
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [4]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gaumatan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity."
QY 1 DIETGSPASLAVSLGGRATISCRASESVDSYGHSEFMQYQKRGOPPKLLIYRASLLEP 60
DB 21 NIYLTGSPASLAVSLGGRATISCRASESVDSYGHSEFMQYQKRGOPPKLLIYRASLLEP 80
QY 61 GIPARFSGSGGTFTLTINPEADVAITYCCQSNEDPFTFGSGTKLEIK 111
DB 81 GVPARFSGSGSRITDFTLTIDPVEADDAITYCCQNNEDPFTFGSGTKLEIK 131

RESULT 4
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01663;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15 kappa chain V-III region PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gaumatan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity."

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RL Nature 276:785-790(1978).  
DR PIR: A01935; KWSM6.  
DR HSSP: P01679; 2EBJ.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 39 53 FRAMEWORK-2.  
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 61 92 FRAMEWORK-3.  
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 102 111 FRAMEWORK-4.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;  
  
Query Match 87.0%; Score 510; DB 1; Length 111;  
Best Local Similarity 87.4%; Pred. No. 2.9e-46;  
Matches 97; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 DIETOSPASLAVSLGQRATISCRASESVDSYGHSMQYQKPGQPKLLIYRASNLKP 60  
DB 1 NIVLTQSPASLAVSLGQRATISCRASESVDSYGHSMQYQKPGQPKLLIYRASNLKS 60  
QY 61 GIPARFSGSGCTDFTLTINPEADVATYYCQGSNEDPFTFGSGTKLEIKR 111  
DB 61 GIPARFSGSGSRBTFTLTIDPEADDAATYYCQGNEDPLTFGACTKLEIK 111  
  
RESULT 5  
KV3F\_MOUSE STANDARD; PRT; 132 AA.  
ID KV3F\_MOUSE  
AC P01658;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region MOPC 321 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP MEDLINE=7823587; PubMed=98179;  
RA Burstein Y., Schechter I.;  
RT "Primary structures of N-terminal extra peptide segments linked to  
RT the variable and constant regions of immunoglobulin light chain  
RT precursors: implications on the organization and controlled  
RT expression of immunoglobulin genes";  
RL Biochemistry 17:2392-2400(1978).  
RN [2]  
RP MEDLINE=73140224; PubMed=4120629;  
RA McKean D.J., Potter M., Hood L.E.;  
RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa  
RT chain";  
RL Biochemistry 12:749-759(1973).  
CC -1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS  
CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT  
CC REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY  
CC RESIDUES.  
DR PIR: A01933; KWS32.  
DR HSSP: P01679; 2EBJ.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region; Bence-Jones protein; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 132 IG KAPPA CHAIN V-II REGION MOPC 321.

FT DOMAIN 21 43 FRAMEWORK-1.  
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 59 73 FRAMEWORK-2.  
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 81 112 FRAMEWORK-3.  
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 122 131 FRAMEWORK-4.  
FT DISULFID 43 112 BY SIMILARITY.  
FT NON\_TER 132 132  
SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BB73FBE9 CRC64;  
  
Query Match 86.7%; Score 508; DB 1; Length 132;  
Best Local Similarity 79.5%; Pred. No. 5.7e-45;  
Matches 89; Conservative 20; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 DIETOSPASLAVSLGQRATISCRASESVDSYGHSMQYQKPGQPKLLIYRASNLKP 60  
DB 21 DIVLTQSPASLAVSLGQRATISCRASKSVNTYGNFMWYZZKPG2PKLLIYRASNLZS 80  
QY 61 GIPARFSGSGCTDFTLTINPEADVATYYCQGSNEDPFTFGSGTKLEIKR 112  
DB 61 GIPARFSGSGSRBTFTLTIDPEADDAATYYCQGNEDPLTFGACTKLEIKR 132  
  
RESULT 6  
KV3G\_MOUSE STANDARD; PRT; 112 AA.  
ID KV3G\_MOUSE  
AC P01659;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region TEPC 124.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP MEDLINE=73140225; PubMed=4691517;  
RA McKean D.J., Potter M., Hood L.E.;  
RT "Mouse immunoglobulin chains. Pattern of sequence variation among  
RT kappa chains with limited sequence differences";  
RL Biochemistry 12:760-771(1973).  
DR PIR: A01933; KWS32.  
DR HSSP: P01679; 2EBJ.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 39 53 FRAMEWORK-2.  
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 61 92 FRAMEWORK-3.  
FT DOMAIN 93 101 FRAMEWORK-4.  
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING-3.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 12339 MW; 7CFD328DBE8E9D71 CRC64;  
  
Query Match 85.5%; Score 501; DB 1; Length 112;  
Best Local Similarity 79.5%; Pred. No. 2.5e-45;  
Matches 89; Conservative 18; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 DIETOSPASLAVSLGQRATISCRASESVDSYGHSMQYQKPGQPKLLIYRASNLKP 60  
DB 1 DIVLTQSPASLAVSLGQRATISCRASZSVNTYGNFMWYZZKPG2PKLLIYRASNLZS 60  
QY 61 GIPARFSGSGCTDFTLTINPEADVATYYCQGSNEDPFTFGSGTKLEIKR 112  
DB 61 GIPARFSGSGSRBTFTLTIDPEADDAATYYCQGNEDPLTFGACTKLEIKR 112

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RESULT 7
KV3M_MOUSE STANDARD: PRT: 111 AA.
ID KV3M_MOUSE
AC P01665:
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 111
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01937; KVM543.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003596; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 FRAMEWORK-2.
FT DOMAIN 39 53 FRAMEWORK-3.
FT DOMAIN 54 60 FRAMEWORK-4.
FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 85.0%; Score 498; DB 1; Length 111;
Best Local Similarity 86.5%; Pred. No. 5, 1e-45;
Matches 96; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGQRTATISCRASESYDSYGHSPMWYQKPGQPKLLIYRASNLDP 60
DB 1 DIVLTQSPASLAVSLGQRTATISCRASESYDSYGHSPMWYQKPGQPKLLIYRASNLDS 60
QY 61 GIPARFSGSGGTFDTLTINPVADVATYTCOQSNEDPFTFGSGTKLEIK 111
DB 61 GIPARFSGSGGTFDTLTINPVADVATYTCOQSNEDPFTFGSGTKLEIK 111

RESULT 8
KV3O_MOUSE STANDARD: PRT: 111 AA.
ID KV3O_MOUSE
AC P01667;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 111
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: C01937; KVM508.
DR HSSP: P80362; 1MTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003006; Ig_V.
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DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 FRAMEWORK-2.
FT DOMAIN 39 53 FRAMEWORK-3.
FT DOMAIN 54 60 FRAMEWORK-4.
FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4DC256D29 CRC64;

Query Match 84.1%; Score 493; DB 1; Length 111;
Best Local Similarity 85.6%; Pred. No. 1, 7e-44;
Matches 95; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGQRTATISCRASESYDSYGHSPMWYQKPGQPKLLIYRASNLDP 60
DB 1 DIVLTQSPASLAVSLGQRTATISCRASESYDSYGHSPMWYQKPGQPKLLIYRASNLDS 60
QY 61 GIPARFSGSGGTFDTLTINPVADVATYTCOQSNEDPFTFGSGTKLEIK 111
DB 61 GIPARFSGSGGTFDTLTINPVADVATYTCOQSNEDPFTFGSGTKLEIK 111

RESULT 9
KV3N_MOUSE STANDARD: PRT: 111 AA.
ID KV3N_MOUSE
AC P01666;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 111
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: B01937; KVM583.
DR HSSP: P01679; 2FBU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 FRAMEWORK-2.
FT DOMAIN 39 53 FRAMEWORK-3.
FT DOMAIN 54 60 FRAMEWORK-4.
FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 83.1%; Score 487; DB 1; Length 111;
Best Local Similarity 83.8%; Pred. No. 7e-44;
Matches 93; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIETOSPASLAVSLGQRTATISCRASESYDSYGHSPMWYQKPGQPKLLIYRASNLDP 60
DB 1 DIVLTQSPASLAVSLGQRTATISCRASESYDSYGHSPMWYQKPGQPKLLIYRASNLDS 60
```



OY 61 GIPARFSGSGSTDFLTINHPVEADVAATYCCQSNEDPFTGSGTKLEIK 111  
 DB 61 GIPARFSGSGSTDFLTINHPVEEDDAATYCCQSNEDPFTGAGTKLEIK 111

RESULT 10  
 KV3Q\_MOUSE STANDARD: PRT: 111 AA.

AC P01669: 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 7769.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;

RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";

RL Nature 276:785-790(1978).  
 DR PIR: E01937; KVM569.

DR HSSP: P80362; 1MTL.

DR InterPro: IPR003006; Ig\_MHC.

DR PIRam: PF00047; 1g; 1.

DR SMART: SM00406; IGV: 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 92 FRAMEWORK-3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 102 111 FRAMEWORK-4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON\_TER 111 111

FT SEQUENCE 111 AA: 12011 MW: 6FAA345279356829 CRC64;

Query Match Best Local Similarity 82.9%; Score 486; DB 1; Length 111;  
 Matches 93; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

OY 1 DIETQSPASLAVSLGQRATISCRASEVSDYSGHSEFMWYQKPGQPKLLIYRASNLSP 60  
 DB 1 DIVLTQSPASLAVSLGQRATISCRASQSVYDGDSDYMNMYQKPGQPKLLIYFASNLSP 60

OY 61 GIPARFSGSGSTDFLTINHPVEADVAATYCCQSNEDPFTGSGTKLEIK 111  
 DB 61 GIPARFSGSGSTDFLTINHPVEEDDAATYCCQSNEDPFTGSGTKLEIK 111

RESULT 11  
 KV3L\_MOUSE STANDARD: PRT: 111 AA.

AC P01664: 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region CBPC 101.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=79012520; PubMed=99744;

RA McKean D.J., Bell M., Potter M.;

RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 RT related mouse kappa variable regions.";

RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
 CC -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

DR PIR: A01936; KVM5C1.

DR HSSP: P80362; 1MTL.

DR InterPro: IPR003006; Ig\_MHC.

DR PIRam: PF00047; 1g; 1.

DR SMART: SM00406; IGV: 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 92 FRAMEWORK-3.  
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 102 111 FRAMEWORK-4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON\_TER 111 111

FT SEQUENCE 111 AA: 11964 MW: E2BIAD98AD965962 CRC64;

Query Match Best Local Similarity 81.9%; Score 480; DB 1; Length 111;  
 Matches 92; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

OY 1 DIETQSPASLAVSLGQRATISCRASEVSDYSGHSEFMWYQKPGQPKLLIYRASNLSP 60  
 DB 1 DIVLTQSPASLAVSLGQRATISCRASQSVYDGESEFMWYQKPGQPKLLIYFASNLSP 60

OY 61 GIPARFSGSGSTDFLTINHPVEADVAATYCCQSNEDPFTGSGTKLEIK 111  
 DB 61 GIPARFSGSGSTDFLTINHPVEEDDAATYCCQSNEDPFTGSGTKLEIK 111

RESULT 12  
 KV3P\_MOUSE STANDARD: PRT: 110 AA.

AC P01668: 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 7210.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;

RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";

RL Nature 276:785-790(1978).  
 DR PIR: D01937; KVM510.

DR HSSP: P01679; 2FBI.

DR InterPro: IPR003006; Ig\_MHC.

DR PIRam: PF00047; 1g; 1.

DR SMART: SM00406; IGV: 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 92 FRAMEWORK-3.  
 FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 101 110 FRAMEWORK-4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON\_TER 110 110

FT SEQUENCE 110 AA: 11950 MW: 69FLASCE86B1249 CRC64;

Query Match Best Local Similarity 79.9%; Score 468.5; DB 1; Length 110;  
 Matches 92; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

OY 1 DIELTOSPASLAVSLGCRATISCRASESYDSYGHSMOWYQOKPGOPPKLLIYRASNLTP 60  
 DB 1 DIELTOSPASLAVSLGCRATISCRASKASQSLDDSDSYMMWYQOKPGOPPKLLIYRASNLTP 60  
 OY 61 GIPARSSGSGGTDFLTINHPVADAVATYCCOQSNEDPFTFGSGTKLEIK 111  
 DB 61 GIPARSSGSGGTDFLTINHPVEEDAVATYCHOS-EDPWTFGSGTKLEIK 110

RESULT 13  
 KV3R\_MOUSE  
 ID KV3R\_MOUSE STANDARD: PRT: 111 AA.  
 AC P01671:  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 7175.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE.  
 RA MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity";  
 RL Nature 276:785-790(1978).  
 DR HSSP; P01938; KWS75.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

Query Match 79.7%; Score 467; DB 1; Length 111;  
 Best Local Similarity 80.2%; Pred. No. 8.4e-42;  
 Matches 89; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

OY 1 DIELTOSPASLAVSLGCRATISCRASESYDSYGHSMOWYQOKPGOPPKLLIYRASNLTP 60  
 DB 1 DIELTOSPASLAVSLGCRATISCRASKASQSLDDSDSYMMWYQOKPGOPPKLLIYRASNLTP 60  
 OY 61 GIPARSSGSGGTDFLTINHPVADAVATYCCOQSNEDPFTFGSGTKLEIK 111  
 DB 61 GIPARSSGSGGTDFLTINHPVEEDAVATYCHOS-EDPWTFGSGTKLEIK 111

RESULT 14  
 KV3R\_MOUSE  
 ID KV3R\_MOUSE STANDARD: PRT: 111 AA.  
 AC P01670:  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 6684.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity";  
 RL Nature 276:785-790(1978).  
 DR HSSP; P01938; KWS84.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;

Query Match 79.4%; Score 465; DB 1; Length 111;  
 Best Local Similarity 81.1%; Pred. No. 1.4e-41;  
 Matches 90; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

OY 1 DIELTOSPASLAVSLGCRATISCRASESYDSYGHSMOWYQOKPGOPPKLLIYRASNLTP 60  
 DB 1 DIELTOSPASLAVSLGCRATISCRASKASQSLDDSDSYMMWYQOKPGOPPKLLIYRASNLTP 60  
 OY 61 GIPARSSGSGGTDFLTINHPVADAVATYCCOQSNEDPFTFGSGTKLEIK 111  
 DB 61 GIPARSSGSGGTDFLTINHPVEEDAVATYCHOS-EDPWTFGSGTKLEIK 111

RESULT 15  
 KV3T\_MOUSE  
 ID KV3T\_MOUSE STANDARD: PRT: 111 AA.  
 AC P01672:  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 7940.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE.  
 RA MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity";  
 RL Nature 276:785-790(1978).  
 DR HSSP; P01938; KWS40.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12038 MW; EE8A82306084352E CRC64;

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Query Match          79.4%; Score 465; DB 1; Length 111;
Best Local Similarity 80.2%; Pred. No. 1.4e-41;
Matches 89; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

OY 1 DIETQSPASLAVSLGQRTATISCRASESVDSYGHSPWYQOKPGQPKLLIYRASNLSP 60
   |||||||||||||||||||:|:|:| ||||||||||| |||
Db 1 DIVLTQSPASLAVSLGQRTATISCRASKSVSAFGSYMHWYQOKPGQPKLLIYLASNLES 60
   |||||||||||||||||||:|:|:| ||||||||||| |||

OY 61 GIPARFSGSGSGTDFTLTINPYEADDVATYYCOQSNEDPFTFGSGTKLEIK 111
   |||||||||||||||||||:|:|:| ||||||| | ||| |||||||
Db 61 GVPARFSGSGSGTDFTLNINHPVEEDAVTYCYCOHSRELPPFTFGSGTKLEIK 111
   |||||||||||||||||||:|:|:| ||||||| | ||| |||||||

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Search completed: January 13, 2003, 15:11:39  
 Job time : 8.27826 secs

